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; Search time 110.536 Seconds (without alignments) 922.194 Million cell updates/sec
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Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Human	Aao19664 Human IgG	GE2 fu	6 Human	Adz69628 Human IgG	Aaw26232 Human IgG	0 Human	Aab80897 Human IgG	Aay72915 Human par	Aae15347 Human imm	2 Human I	1 Herpes	Adj57512 Human IgG	2 Human	6 Human	7 Novel	Human	Adv99720 Human IgG	Human	Human	Human	Aea88761 Human IgG	Abb09463 Human IgG	Ady22146 Human imm
SUMMARIES	ar ar	AA019665	AA019664	AA019668	ADZ87506	ADZ69628	AAW26232	AAB28690	AAB80897	AAY72915	AAE15347	AAE26272	ADJ65991	ADJ57512	ADR48992	ADU51146	ADW39127	ADV91799	ADV99720	ADY55884	ADZ86538	AEA18941	AEA88761	ABB09463	ADY22146
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ALIGNMENTS

AA019665 standard; protein; 232 AA

RESULT 1 AAO19665 AA019665;

The present invention relates to a fusion molecule comprising a first polypeptide sequence capable of specific binding to a native IgG inhibitory receptor consisting of an immune receptor tyrosine-based inhibitory motif (ITIM), expressed on mast cells, basophils or B cells, functionally connected to a second polypeptide sequence capable of specific binding directly or indirectly to a native IgE receptor (FcepsilonR). Also provided are nucleotide sequences encoding such a New fusion molecules comprising polypeptide sequences that bind to IgG inhibitory receptor and native IgE receptor, useful for treating IgE-mediated hypersensitivity reactions, e.g. asthma or allergies, or chain; Human; IgG1; immunoglobulin G; immunotherapy; immune disease; Fcepailon receptor; autoimmune disease; constant region; heavy antiasthmatic; antiallergic; antinflammatory; dermatological; antiarthritic; antirheumatic; antidiabetic; neuroprotective; Human IgG1 heavy chain constant region hinge-CH2-CH3 portion. Claim 19; Fig 3; 116pp; English. 01-MAY-2002; 2002WO-US013527. 01-MAY-2001; 2001US-00847208. 24-OCT-2001; 2001US-00000439. ä (first entry) Zhu (REGC) UNIV CALIFORNIA. hinge-CH2-CH3 region WPI; 2003-103456/09. autoimmune diseases. Saxon A, Zhang K, WO200288317-A2. Homo sapiens. 28-MAR-2003 07-NOV-2002.

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ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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fusion protein. The fusion molecules and compositions are useful for treating an IGE-mediated biological response, preferably an IGE-mediated hypersensitivity reaction, such as sathma, allergic rhinitis, atopic dermatitis, severe food allergies, chronic urticaria, angioedema or anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis, type-I diabetes mellitus, or multiple sclerosis, and for preventing of, or symptoms resulting from, a type I hypersensitivity reaction in a subject receiving immunotherapy. The present sequence is the human IgGI heavy chain constant region hinge-CH2-CH3 portion
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100.0%; Pred. No. 3.3e-91;
iive 0; Mismatches 0;
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24-OCT-2001; 2001US-00000439.
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Best Local Similarity
Matches 232; Conserv
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The present invention relates to a fusion molecule comprising a first

Claim 64; Fig 2; 116pp; English.

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polypeptide sequence capable of specific binding to a native IgG inhibitory receptor consisting of an immune receptor tyrosine-based inhibitory motif (ITIM), expressed on mast cells, basophils or B cells, functionally connected to a second polypeptide sequence capable of specific binding directly or indirectly to a native IgE receptor (FcepsilonR). Also provided are nucleotide sequences encoding such a fusion protein. The fusion molecules and compositions are useful for treating an IgE-mediated biological response, preferably an IgE-mediated hypersensitivity reaction, such as asthma, allergic rhinitis, atopic dermatitis, severe food allergies, chronic urticaria, angioedema or anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis, crype-I diabetes mellitus, or multiple sclerosis, and for preventing of or symptoms resulting from, a type I hypersensitivity reaction in a subject receiving immunotherapy. The present sequence is the human IgGI
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Rcepsilon receptor; autoimmune disease; constant region, heavy chain;
antiasthmatic; antiallergic; antiinflammatory; dermatological; GE2;
antiathritic; antirheumatic; antidiabetic; neuroprotective;
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ive 0; Mismatches 0;
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The present invention relates to a fusion molecule comprising a first polypeptide sequence capable of specific binding to a native IgG inhibitory receptor consisting of an immune receptor tyrosine-based inhibitory motif (ITIM), expressed on mast cells, basophils or B cells, cunctionally connected to a second polypeptide sequence capable of specific binding directly or indirectly to a native IgB receptor (Repsilona). Also provided are nucleotide sequences encoding such a fusion protein. The fusion molecules and compositions are useful for treating an IgE-mediated biological response, preferably an IgE-mediated Mypersensitivity reaction, such as asthma, allergic rhinitis, atopic dermatitis, severe food allergies, chronic urticaria, angicedema or anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis, type-I diabetes mellitus, or multiple sclerosis, and for preventing of, or symptoms resulting from, a type I hypersensitivity reaction in a subject receiving immunotherapy. The present sequence is a gammahinge-CHgamma2-CHgamma3-(Gly4Ser)3-CHepsilon2-CHepsilon3-CHepsilon3 fusion trotein (designated GE2) of the invention
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fusion molecules comprising polypeptide sequences that bind to IgG bitory receptor and native IgE receptor, useful for treating IgE-ated hypersensitivity reactions, e.g. asthma or allergies, or
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                                                                                     7; 116pp; English
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12-NOV-2003; 2003US-0519822P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 232; Conservative
                                                     autoimmune diseases.
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                                                                                                                                                                     This invention relates to a novel MUC1 chimeric protein which comprises a first polypeptide sequence and a second polypeptide sequence, where the first polypeptide sequence is a MUC1 extracellular (MUC1-EC) polypeptide, and the second polypeptide sequence is a human immunoglobulin FC polypeptide or a human abumin polypeptide. The invention may be useful for the development of compounds with a cytostatic activity acting as MUC1 antagonists or CD27 antagonists. The MUC1 chimeric protein is useful in preparing a composition for treating cancer. The present sequence is that of a protein which was used during the development of the novel MUC1 chimeric protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                  MUC1 ligand trap comprising a MUC1 extracellular polypeptide and an immunoglobulin FC polypeptide or an albumin polypeptide, useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
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                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human IgG1 heavy chain constant region, mutant L314M.
                                                                                                                                                                                                                                                                                                                                                                        97.8%; Score 1232; DB 9;
97.4%; Pred. No. 5.4e-89;
tive 3; Mismatches 3;
                                                                                                                                             Disclosure; SEQ ID NO 33; 82pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
           Kharbanda S, Kufe DW
                                        2005-346855/35.
                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                       N-PSDB; ADZ87507
                                                                                                                                                                                                                                                                                                                                               Sequence 232 AA;
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Synthetic.
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Matches 226;
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AAW26232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New modified Fc-fusion protein where at least one amino acid residue from the heavy chain constant region, useful for studying protein function in vitro and in vivo and as potential therapeutic and diagnostic agents.
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Pred. No. 1.7e-88;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 21; SEQ ID NO 29; 170pp; English.
                                                                                                                                                           (PROT-) PROTEIN DESIGN LABS INC.
15-OCT-2003; 2003US-0511687P.
14-APR-2004; 2004US-0562627P.
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                                                                                                                                                                                                                                                                  Hinton PR,
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Best Local
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A novel recombinant vector has been developed which comprises a nucleotide sequence encoding a fusion protein. The fusion protein comprises three domains joined together in order, from N-terminus to terminus, of a first domain comprising a protein of interest, a second domain comprising an hydrophilic spacer and an affinity domain, each domain comprising amino acid residues. The present sequence represents the hinge/Fc region of human 19G1, used in example 3 of, the present invention. The recombinant vector is used for the production of authentic recombinant proteins of interest. The method of the invention is useful for the expression of fusion proteins capable of isolation by affinity chromatography in pro- or eukaryotic cells. This method allows for the efficient cleavage and generation of authentic proteins of interest that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant protein expression system for fusion protein production - useful for high quantity production of authentic recombinant proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        do not contain extraneous (i.e. non-naturally occurring) amino acids
                                                                                                                                        Fusion protein; hydrophilic spacer; recombinant; expression system; carboxypeptidase; IgG1; immunoglobulin; hinge region; Fc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PVLDSVGSFFLYSKLIVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 97.2%; Score 1225; DB 2; Best Local Similarity 97.0%; Pred. No. 1.9e-88; Matches 225; Conservative 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Page 133-134; 194pp; English.
AAW26232 standard; protein; 232 AA.
                                                                                                                                                                                                                                                                                                            97WO-US001470.
                                                                                                                                                                                                                                                                                                                                              96US-00595043.
                                                                                                         Human IgG1 hinge/Fc region.
                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                  (TECH-) TECHNOLOGENE INC
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N-PSDB; AAT80158.
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                                                                                                                                                                                                  sapiens.
                                                                                                                                                                                                                                                                                                            31-JAN-1997;
                                                                                                                                                                                                                                    WO9728272-A1
                                                                                                                                                                                                                                                                                                                                              31-JAN-1996;
                                                                                                                                                                                                                                                                        07-AUG-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                    Sgarlato GD;
                                                                       16-MAR-1998
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                                   AAW26232;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence was used in the production of AGP-1 fusion proteins. AGP-1 is a type II transmembrane protein. The fusion proteins comprise an PC immunoglobulin region fused to the N-terminal portion of the AGP-1 protein. The fusion proteins can be used to induce apoptosis in a tissue, and to treat proliferative disorders, immune disorders, or virally-induced disorders. The proliferative disorders include cancers, such as breast, prostate, lung or colon cancer. The viral infections include hepatitis, and acquired immunodeficiency syndrome (AIDS), and the immune disorders may be autoimmune disorders or transplant rejection.
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                                                                                                                                                Human, AGP-1; type II transmembrane protein; cytostatic; antiviral; antiinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV; human immunodeficiency virus; apoptosis; proliferative disorder; cancer; hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder; transplant rejection; cardiovascular disease; arteriosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NWYVDGVEVHNAKTKPREEGYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fusion protein of AGP-1 protein and an Fc region, used to treat
proliferative disorders, immune disorders, and virally-induced disorders.
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                                                                                                                Human IgGgammal hinge, CH2 and CH3 regions.
       AAB28690 standard; protein; 232 AA
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                                                                              (first entry)
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                                                                              14-FEB-2001
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The present invention relates to a method for the prevention or treatment of lytic bone disease or multiple myeloma. Also the method can be used for preventing metestasis of cancer to bone or osteosclerotic bone metastasis. The method comprises administering an OPG (osteoprotegrin) polypeptide or OPG fusion protein. The OPG proteins (see AAB80898-AAB80965) can inhibit formation of osteoolasts (and thus bone resorption) by blocking differentiation from monocytes/macrophage precursors. The present sequence is the hinge, CH2 and CH3 regions of human IgGgammal. This sequence can be used to generate fusion proteins of OPG and immunoglobulin, for use in the present invention. The generated fusion proteins can exhibit increased circulating half-lives and slower clearance times, thereby providing a more sustained activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Preventing or treating lytic bone diseases, particularly associated with cancer or metastasis, by administering an osteoprotegrin polypeptide.
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1.9e-88;
                                                                                                                                                                                                                                                                                 osteoclast formation inhibition; bone resorption inhibition
                                                                                                                                                                                                     Human, IgGgammal, anticancer, Antimetastatic, Osteoger
lytic bone disease, multiple myeloma, immunoglobulin,
osteosclerotic bone metastasis, OPG; osteoprotegrin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                   Human IgGgammal hinge, CH2 and CH3 regions.
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Pred. No. 1.
AAB80897 standard; protein; 232 AA.
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                                                                                                     (first entry)
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Matches 225; Conservative
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Best Local Similarity
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                                                   AAB80897;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The patent discloses fusion protein comprising human osteoprotegerin (OPG) protein fused by linker to human 1961 Fc portion. OPG negatively regulates formation of osteoclasts in vitro and in vivo. It blocks the differentiation of osteoclasts from monocyte or macrophage precursors and the reabsorption of bone. The OPG-Fc fusion protein is administered for the treatment of bone loss resulting from osteoporosis, Paget's disease, osteomyelitis, hypercalcaemia, osteopenia associated with surgery or steroid administration, osteonecrosis, bone loss due to rheumatoid arthritis, periodontal bone loss, osteolptic metastasis and/or prosthetic loosening. The present sequence is partial human immunoglobulin G (Ig G) i protein comprising the hinge and heavy chain constant regions CH2 and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Osteoprotegerin-Fc protein fusions useful for treating bone loss caused by e.g. osteoporosis, Paget's disease and osteomyelitis.
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                                                                                                                                  Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic; therapy; bone loss; osteoprofais; paget's disease; osteomelitis; hypercalcaemia; osteopenia; osteonerosis; rheumatoid arthritis; osteolytic metastasis; prosthetic loosening; immunoglobulin d1; IgG1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                    Human partial IgG1 protein comprising hinge, CH2 and CH3 regions.
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97.0%; Pred. No. 1.9e-88;
iive 3; Mismatches 4;
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AAY72915 standard; protein; 232
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                                                                   (first entry)
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Best Local Similarity 97.0
Matches 225; Conservative
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                                 AAY72915
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The invention relates to a method for increasing and maintaining haematocrit in a mammal. The method comprises administering a hyperglycosylated analogue of erythropoletin (Bpo) in a pharmaceutical composition, less frequently than an equivalent molar amount of and at a lower molar amount than recombinant human Bpo (rHuBpo) to obtain a comparable target heamatocrit. Bpo is a glycoprotein hormone necessary for the maturation of erythroid progenitor cells into erythrosytes. Human Bpo analogue is useful for raising and maintaining haematocrit to a comparable target heamatocrit in a mammal suffering from anaemia associated with a decline or loss of kidney function, myelosuppressive therapy comprising chemotherapeutic or anti-viral drugs or associated with excessive blood loss during surgical procedures, and in cancer condition. The present sequence is human immunoglobulin G (IgG) gamma 1 constant heavy chain (CH2, CH3) hinge region used to construct Bpo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Increasing and maintaining hematocrit in mammal suffering from anemia, comprising administering hyperglycosylated analog of erythropoietin less frequently and at lower molar amount of recombinant human erythropoietin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                  Human, erythropoietin, Epo, haematocrit, anaemia, kidney function, 1gG;
cancer, myelosuppressive therapy, anti-viral drug, immunoglobulin G.
                                                                                                                                                                                                                   Human immunoglobulin G (IgG) gamma 1 constant heavy chain hinge region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPFKPKDTLMISRTPEVTCVVVDVSHEDDEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 BPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 97.2%; Score 1225; DB 5; Length 232; Best Local Similarity 97.0%; Pred. No. 1.9e-88; Matches 225; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sitney KC;
AAE15347 standard; protein; 232 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Browne JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 10; 95pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-APR-2001; 2001WO-US012836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-APR-2000; 2000US-00559001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Elliott SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-034433/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 232 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200181405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                09-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Egrie JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
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                                                                          AAE15347;
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11

RESULT

RESULT 10 AAE15347

ð 유 ò g 8 엄 ò 181 PVLDSDGSFPLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232

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ADJ65991 standard; protein; 232

RESULT 12

ADJ65991

PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK

181

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232

ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180

g

8

1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT

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The invention relates to a compound comprising an immunoglobulin (Ig)

Control of the capable of binding an amyloidogenic protein. The invention is peptide capable of binding an amyloidogenic protein. The invention is peptide capable of binding an amyloidogenic protein. The invention is consetul for clearing an amyloidogenic protein protein in the invention is peptide capable of binding an amyloidogenic protein in the invention is consetul for clearing an amyloidogenic protein with anyloid polypeptide (TARP), atrial natriuretic factor (ARP), islet amyloid polypeptide (TARP), atrial natriuretic factor (ARP), islet amyloid polypeptide (TARP), atrial natriuretic factor (ARP), sappa light chain, lambda light chain, amyloid a publect and for treating an amyloidogenic disorder such as Alzheimer's disease and spongiform encephalopathy. Disorders treatable anyloid cardiomyopathy), PPP (eg. spongiform encephalopathies, including creapie in sheep, bovine spongiform encephalopathies, including creapie in sheep, bovine spongiform encephalopathies, including creapie in sheep, bovine spongiform encephalopathy in cows and creating anyloid sease (CJ) and derstmann-Straussler-Scheinker creating anyloidosis, myeloma), amyloid A (eg. amyloidosis), Apo A-I (eg. hereditary non-neuropathic systemic amyloidosis), Gelsolin (eg. familial amyloidosis of Finnish type), Fibrinogen (eg. hereditary renal amyloidosis of Fibrinish type), Fibrinogen (eg. hereditary renal amyloidosis of Fibrinish type), Fibrinogen (eg. hereditary renal amyloidosis of
                                                                                                                                                                                                                      Human, amyloidogenic protein, Alzheimer's disease, Huntington's disease, spongiform encephalopathy; familial amyloid cardiomyopathy; amyloidosis, Gerstmann-Straussler-Scheinker syndrome; spongiform encephalopathy; 36S5, Creutzfeldt-Jacob disease, insulinoma; diabetes; body myocytis; myeloma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel therapeutic agent useful for treating an amyloidogenic disorder, e.g. Alzheimer's disease, comprises an immunoglobulin heavy chain constant region linked to a peptide capable of binding amyloidogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.2%; Score 1225; DB 5; Length 232; 97.0%; Pred. No. 1.9e-88; ive 3; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gosselin
                         AAE26272 standard; protein; 232 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Joyal JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 8; Page 76; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-NOV-2000; 2000US-0253302P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0250198P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-NOV-2001; 2001WO-US044581.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-DEC-2000; 2000US-0257186P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PRAE-) PRAECIS PHARM INC.
                                                                                                                         (first entry)
                                                                                                                                                                          Human IgG1 heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gefter ML, Israel DI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-636427/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 232 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            WO200242462-A2.
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                           14-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2002
                                                                          AAE26272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein.
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NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention comprises a therapeutic agent for treating endotoxin induced disease, the therapeutic agent contains a fusion protein of the Herpes virus entry mediator (HVEM) protein and an immunoglobulin Fo domain. The therapeutic agent of the invention is useful for treating endotoxin induced disease, such as endotoxic shock. The present amino acid sequence represents a human protein which is claimed in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISKTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       peutic agent, useful for treating endotoxin induced disease, fusion protein of Herpes virus entry mediator protein and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                            therapeutic agent; endotoxin induced disease; fusion protein; Herpes virus entry mediator; HVEM; immunoglobulin Fc domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 7; Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1225; DB 7;
Pred. No. 1.9e-88;
3; Mismatches 4
                                                                                 Herpes virus entry mediator-related protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; SEQ ID NO 2; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.2%;
                                                                                                                                                                                                                                                              25-OCT-2001; 2001JP-00328430
                                                                                                                                                                                                                                                                                          25-OCT-2001; 2001JP-00328430
                                                      06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 225; Conservative
                                                                                                                                                                                                                                                                                                                    (TAIS ) TAISHO PHARM CO (GENE-) GENE TECHNO SCI
                                                                                                                                              endotoxic shock; human.
                                                                                                                                                                                                                                                                                                                                                                                                            New therapeutic agent,
                                                                                                                                                                                                                                                                                                                                                              2003-817833/77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ADJ65998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 232 AA;
                                                                                                                                                                                                      JP2003128576-A.
                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                 08-MAY-2003.
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                         ADJ65991;
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Query Match
Best Local Similarity 97.0
Matches 225; Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a compound (I) binding to tissue factor (TF).

The compound (I) has the formula A-(LM)-C, where A is a FVIIa polypeptide, LM is an optional linker group, C comprises an impurpational to the group, C comprises an impuratory effector domain, and (I) binds to TF. (I) inhibits TF-mediated activated factor VII (FVIIa) activity. (I) is useful as a medicament, and for the manufacture of a medicament for preventing or treating disease or disorder associated with pathophysiological TF activity. The disease or disorder associated with pathophysiological TF activity are deep venous thrombosis, arterial thrombosis, post surgical thrombosis, coronary artery bypass graft (ARBG), percutaneous transdermal coronary angloplastry (PTCA), stroke, cancer, tumor metastasis, and restenosis following angloplastry, acute and chronic indications such as inflammation, septic shock, septicemia, hypotension, adult respiratory distress syndrome (ARDS), disseminated intravascular cagulopathy (DIC), pulmonary embolism, platelet deposition, myocardial infarction, or prophylactic treatment of mammals with atherosclerotic vessels at risk for thrombosis. The present sequence represents the Fc domain fragment of human immunoglobulin GI (19GI).
                                          180
                                                                                                                                                                                                                                                                                                                                                                                           TF; tissue factor; FVIIa; factor VII; anticoagulant; thrombolytic; erebroprotective; oytostatic; vasotropic; antirheumatic; antiarthritic; antiarteriosclerotic; antiinflammatory; antibacterial; immunosuppressive; hypertensive; cardiant; coagulation Factor VII; human; immunoglobulin G1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ompound binding to tissue factor, useful for treating diseases such angiogenesis, ischemia/reperfusion, and rheumatoid arthritis.
                                ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                   232
                                                                                                        PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                   PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.2%; Score 1225; DB 8; Length 232; 97.0%; Pred. No. 1.9e-88; ive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Steenstrup TD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 16; SEQ ID NO 7; 61pp; English
                                                                                                                                                                                                                              ADJ57512 standard; protein; 232 AA
                                                                                                                                                                                                                                                                                                                                                      Human IgG1 Fc domain fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JUL-2003; 2003WO-DK000481.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-JUL-2002; 2002DK-00001099.
                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nicolaisen EM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NOVO ) NOVO NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-180224/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 232 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2004006962-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-JAN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bjorn SE,
                                                                                                                       181
                                                                                                                                                                                                                                                                       ADJ57512;
                                        121
                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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CHUEPO), a peptide linker, and a human 19G Fc variant, is new.

CHUEPO), a peptide linker, and a human 19G Fc variant, is new.

CHUEPO, a peptide linker, and a human 19G Fc variant, is new.

CHOSTORIANS are also included for the following: a chinese hamster

COVATY (CHO)-derived cell line producing the HUEPO-L-VFC fusion protein in

its growth medium in excess of 10 kmicro;g per million cells in a 24 hour

period; and a method for making a recombinant fusion protein comprising

HUEPO, a flexible peptide linker, and a human 19G Fc variant. Preferred

Protein: The peptide linker containing 20 or fewer amino acids is present

between HUEPO and the human 19G Fc variant, and comprises two or more

amino acids selected from glycine, serine, alanine, and threonine. The

human 19G Fc variant comprises a hinge, CH2, and CH3 domains of human

19G2 with Pro311Ser mutation comprising 436 amino acids (SEQ ID NO. 18).

It also comprises a hinge, CH2, and CH3 domains of human 19GH with

Ser228Pro and Leu235Ala mutations comprising 437 amino

20). It further comprises a hinge, CH2, and CH3 domains of human 19GH

with Leu234Val, Leu235Ala mutations comprising 435 amino

cids (SEQ ID NO. 22). The HUEPO-L-VFC fusion protein exhibits in vitro

biological activity similar to or higher than that of rHuEPO on a molar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin (HuEPO), a peptide linker, and a human 1gG Fc variant, useful for treating chronic anemia due to renal diseases, cancer chemotherapy, or
                                                                                                                                                                180
                                                                                                                                                                                                         121 ISKAKGÓPREPÓVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antianaemic; nephrotropic; human; HuEPO-L-vFc; erythropoietin; EPO; anaemia; renal disease; cancer chemotherapy; rheumatoid arthritis; AZT treatment; HIV infection; myelodysplastic syndrome; renal failure.
BPKSCDKTHTCPPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVDDVSHEDPEVKF
                                                                                                                61 NWYVDGVEVHNAKTKPREBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                   121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                        61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                    181 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVWHEALHNHYTQKSLSLSPGK 232
                                                                                                                                                                                                                                                            181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 26; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                          ₹.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human 1gG1 hinge and CH2 region.
                                                                                                                                                                                                                                                                                                                                                                                                                          ADR48992 standard; peptide; 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-AUG-2001; 2001US-00932812.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JAN-2004; 2004US-00761593.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sun CRY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-634851/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUN L K.
SUN B N C.
SUN C R Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sun LK, Sun BNC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2004175824-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADR48992;
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Conservative

Similarity

Local Simi hes 225;

Best Loca Matches

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9

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and incorporates a Bamil site. The resulting DNA fragments of approximately 600 bp were inserted into a holding vector such as pUC19 at the HindIII and Bamil sites to give the pEPO plasmid. The sequence of the human EPO gene was confirmed by DNA sequencing.
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Sequence 232 AA;

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                                                                                                            NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                  ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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                                                                       1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPFKFKDTLMISRTPEVTCVVVDVSHEDFEVKF
                                                                                                                             EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                             Gaps
                                                                                                                                                                                                                                        PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
                                                                                                                                                                                                                        PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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0
Score 1225; DB 8; Length 232;
Pred. No. 1.9e-88;
3; Mismatches 4; Indels (
  97.2%;
97.0%;
Query Match
Best Local Similarity 97.0
Matches 225, Conservative
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120 9

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ADU51146 standard; protein; 232 AA
ADU51146
   X S X & & X E X B X B X B X B
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Search completed: November 30, 2005, 00:51:22 Job time : 113.536 secs

ADUS1146;

(first entry)

27-JAN-2005

Human spleen-expressed receptor-related solubility-promoting protein.

immunosuppressive; cytostatic; antiinflammatory; immune modulation; intercellular communication; autoimmune disease; cancer; neoplasm; transplant rejection; immune disorder; inflammation; gene therapy.

Homo sapiens

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121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel purified polypeptide comprising any of SEQ ID NOs: 3, 7, 9, 11, 45 or 88, or an amino acid sequence that is 95% or more identical to the amino acid sequences and which includes an immunoglobulin like domain structure. The polypeptide of the invention demonstrates immunosuppressive, cytostatic and antiinflammatory activities and is a splean-expressed (SPEX) polypeptide. The methods and compositions of the present invention may useful for modulating lymphocyte activation and the immune response in a variety of conditions lincluding autoimmunity, cancer, transplant rejection and inflammation. Such modulation may be achieved via the use of gene therapy. The current sequence is that of the human spleen-expressed (SPEX) receptor-related
                                                                                                                                                                                                                                                                                New purified spleen expressed (SPEX) polypeptide useful for modulating lymphocyte activation and the immune response in disorders including autoimmunity, cancer, transplant rejection and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EPKSCDKTHTCPPCPAPELLGGPSVPLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.2%; Score 1225; DB 8;
ilarity 97.0%; Pred. No. 1.9e-88;
Conservative 3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      solubility-promoting protein of the invention.
                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 97; 98pp; English.
                                                                                                                                                             GMBH.
                                                                    29-APR-2004; 2004WO-EP004562
                                                                                                         30-APR-2003; 2003US-0467206P
                                                                                                                                        (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS PHARMA GI
(SCRI ) SCRIPPS RES INST.
                                                                                                                                                                                                                Kaye J, Wilkinson B;
                                                                                                                                                                                                                                                    WPI; 2004-804740/79.
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Matches 225; Conserv
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WO2004096976-A2
                                   11-NOV-2004
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(otqsu) Anole Blank (uspto)

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                    Copyright
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sw model using protein search, protein ξ

November 30, 2005, 00:46:45; Search time 21.8551 Seconds (without alignments) 1021.378 Million cell updates/sec Run on:

Title: Perfect

US-09-847-208B-3 1260 1 EPKSCDKTHICPPCPAPELL......MHEALHNHYQQRSLSLSPGK 232 score: Sequence:

Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched: of hits satisfying chosen parameters: Total number

length: 0 length: 2000000000 seq 08 08 Minimum I Maximum I

summaries Post-processing: Minimum Match 0% Maximum Match 100 Listing first 45

PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Ig gamma-1 chain C	ᆽ	Ig gamma-1 chain C	Ig gamma chain C r	chain		heavy	chain	chain	þa	ρ	σ				Ig gamma 3 chain c	Ъ	Ig gamma-2b chain	Ig gamma-3 chain C	Ig heavy chain C r				gamma-1 chain	gamma-1 chain		-2c	g gamma-2a cha	Ig gamma-2a chain
ID	СННО	869339	S31866	PT0207	A23511	A60764	G3HUWI	G2HU	G4HU	GHRB	147160	147159	147162	G2GP	147158	147161	S22080	PS0018	G3MSC	C30554	S31459	G3MSM	PC4436	G1MS	PS0017	GIMSM	S00847	G2MSA	S37483
ength DB	330 1	374 2	255 4	4	377 2		289 1	326 1	327 1	323 1	328 2	328 2	277 2	329 1	328 2	328 2	470 2	333 2	329 1	308 2	472 2	•	•	324 1	···	393 1	329 2	330 1	469 2
% Query Match Length	97.2	7.96	96.6	93.0	90.3	90.2	89.1	87.9	87.1	70.1	68.9	68.9	8	68.1	67.3	66.7	65.1	64.5	64.5	64.4	64.4	63.6	63.1	62.7	62.3	62.3	61.6	61.6	61.6
8	1225	1219	1217	1172	1138	1136	1123	1107	1097	883	868.5	œ	œ	858	847.5	840.5	820	813	812.5			801.5		789.5	784.5	784.5		776	116
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Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2b chain	Ig gamma-2a chain	Ig gamma-2b chain	Ig gamma-2 chain C	Ig gamma-2b chain	Ig gamma heavy cha	Ig heavy chain VHI	Ig heavy chain V-I	Ig gamma-1 chain C	Ig Y heavy chain (Ig heavy chain pre	Ig mu chain C regi	Ig mu chain C regi
G2MSAB	G2MSAM	S40295	G2MS11	PS0019	GZMSBM	806611	S01321	146732	S69340	A36040	S14236	B46529	S04845	S25644	MHMS
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335	399	446	474	322	405	327	475	180	249	218	152	572	549	343	455
61.3	61.2	60.4	59.6	59.3	59.2	58.3	58.1	53.1	43.6	43.4	43.0	29.1	28.3	28.0	28.0
772	771	761	751.5	747.5	746.5	735	731.5	699	549	547	542	366.5	357	353	353
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Ig gamma-1 chain C region - human C;Species: Homo sapiens (man) (C;Species: Homo sapiens (man) (C;Species: Homo sapiens (man) (C;Species: Homo sapiens (man) (C;Species: Homo-1982 #text_change 09-Jul-2004 (C;Accession: A93433; S36861: B91867; B90563; A90564; B91668; A91723; A02146 R;Ellison, J.W.; Berson, B.J.; Hood, L.E. Nucleic Acids Res. 10, 4071-4079, 1982 (A;Title: The nucleotide sequence of a human immunoglobulin C-gammal gene. A;Reference number: A93433; MUID:82274238; PMID:6287432

A; Molecule type: DNA A; Residues: 1-330 <ELL.) A; Cross-references: UNIPROT: PO1857; UNIPARC: UPI0000034COB; EMBL: Z17370 A; Cross-references: UNIPROT: PO1857; UNIPARC: UPI0000034COB; EMBL: Z17370 A; Note: this sequence has the Gim(17) allotypic marker, 97-Lys, and the Gim(1) markers, A; Note: Lys-330 is removed after translation A; Note: Lys-330 is removed after translation Bubmitted to the EMBL Data Library, October 1992 A; Reference number: S33904

A, Accession: S36861

A;Molecule type: DNA A;Residues: 2-330 cHAR> A;Cross-references: UNIPARC:UPI000013C6FE; EMBL:Z17370 A;Cross-references: UNIPARC:UPI000013C6FE; EMBL:Z17370 R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T. Cell 29, 671-679, 1982 A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a A;Reference number: S33887; MUID:83001943; PMID:6811139

A; Molecule type: DNA
A; Residues: 88-113;235-330 <TAK>
A; Residues: 88-113;235-330 <TAK>
A; Residues: 88-113;235-330 <TAK>
A; Residues: Ba-113;235-330 <TAK>
A; Cross-references: UNIPARC:UPT000017378B; UNIPARC:UP1000017378C; EMBL:Z17370
B; Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, B; Cunningham, B.A.; Rutishauser, U.; Gall, M.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, A; Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seque# A; Reference number: A90563; MUID:71064024; PMID:5489771
A; Contents: myeloma protein Eu
A; Accession: B90563

A,Molecule type: protein
A,Molecule type: protein
A,Residues: 1-96, R.,98 1-315 < CUN>
A,Residues: 1-96, R.,98 1-315 < CUN>
A,Cross-references: UNIPARC:UPI000017378D
A,Ocross-references: UNIPARC:UPI000017378D
A,Note: this sequence has the Glm(3) marker, 97-Arg
B;Rutishauser, U; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A,Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequé
A;Reference number: A90564; MUID:71064025; PMID:5530842

A; Accession: A90564

A; Modecule type: protein A; Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240, A; Cross-references: UNIPARC:UPI000017378E A; Note: this sequence has the GIM(non-1) markers, 239-Glu and 241-Met R; Ponstingl, H:; Hilschmann, N.

N

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Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
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                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140,'C',142-374 <KH2>
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Local Similarity 96.6%;
les 224; Conservative
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Best Local S:
Matches 224
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                                                                A,Reference number: A91668, MUID:77070269; PMID:826475
A,Contents: myeloma protein Nie
A,Accession: B91668
A,Accession: B91668
A,Molecule type: protein
A,Residues: 1-34, Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27
A,Cross-references: UNIPARC:UPI000017378F
A,Cross-references: UNIPARC:UPI000017378F
A,Note: this sequence has the G1m(17) and G1m(1) markers
R,Schmidt, W.E.; Jung, H.D.; Palm, W, Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A,Title: Die Primaerstruktur des Kristallisierbaren monoklonalen Immunglobulins IgG1 KOI
A,Reference number: A91723; MUID:83289313; PMID:6884994
A,COntents: myeloma protein KOL; disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Accession: M91723
A, Molecule type: protein N01, 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A, Molecule type: protein
A, Molecule type: protein
A, Residues: 1-96, 'R', 98-197
A, Order this sequence has the Glm(3) and Glm(non-1) markers
A, Note: this sequence has the Glm(3) and Glm(non-1) markers
B, Gall, W.E.; Edelman, G.M.
B, Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A, Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A, Totherts: annotation; disulfide bonds
B, Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A, Phylie: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob enbromide cleavage products, and the disulfide bridges.
A, Reference number: A91667; MUID: 77070267; PMID: 1002129
A, Contents: annotation; disulfide bonds
C, Genetics: annotation; disulfide bonds
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A:Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie).
igen Primaerstruktur.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 EPKSCOKTHICPPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
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97.0%; Pred. No. 1.7e-85;
iive 3; Mismatches 4;
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es 225; Conser
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Ig heavy chain V region precursor - human C; Species: Homo sapiens (man)

RESULT 2 S69339

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A;Description: Screeing method for protein-protein interactions of cloned gene products. A;Description: Screeing method for protein-protein interactions of cloned gene products. A;Description: S31866
A;Accession: S31866
A;Accession: S31866
A;Molecule type: mRNA
A;Residues: 1-255
A;Cross-references: UNIPARC:UPI000011F41F; EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID: C;Keywords: immunoglobulin
F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: bumman Ig gamma-1 chain C region
Cincession: S69339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease. A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
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C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C;Accession: $31866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 NWYYDGVEVHNVKTKPREEQYNSTYRVVSVLTVIHQNWMNGKEYKCKVSNKALPAPIEKT
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
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Pred. No. 4.9e-85;
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RESULT 4

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Iggamma-3 heavy chain disease proteins - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999 C;Accession: A90442; A9219; A90198; A93915; A02149 R;Prandjone, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C. Biochemistry 19, 4304-4308, 1980 A;Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-A;Contents: heavy chain disease protein Wis A;Contents: heavy chain disease protein Wis A;Accession: A90442 A;Accession: A90442 A;Accession: A90442 A;Accession: A;
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C;Species: Howo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 31-Dec-2004
C;Datesion: A60764
B;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an 1
A;Reference number: A60764; MUID:90007613; PMID:2571587
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                                                                                                         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
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C;Superfamily: Ammunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>
13;
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; Pred. No. 1.1e-78;
11; Mismatches 13;
Mismatches
11;
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89.7%;
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Matches 208; Conservative
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A;Molecule type: DNA
A;Residues: 1-377 <HUC>
   208;
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Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Accession: A23511
Ribuck, S.; Bort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: cc
A;Reference number: A23511; MUID:86148507; PMID:3081877
A;Reference number: A23511
A;Molecule type: DNA
A;Residues: 1-377 cHUC>
A;Residues: 1-377 cHUC>
A;Residues: 1-377 cHUC>
A;Coss-references: UNIPARC:UPI000004718F; GB:X03604; GB:M12958; NID:g33070; PIDN:CAA272
A;Genetics GB:IGHG3
A;Cross-references: GDB:119339; OMIM:147120
                                                                                                                                                                                                                                                                                                                                                                                                              Iggamma chain C region - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Species: Pan troglodytes (chimpanzee)
C;Species: Pan troglodytes (chimpanzee)
C;Accession: PT0207
R;Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A;Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A;Reference number: PT0207; MUID:91287716; PMID:2062315
A;Accession: PT0207
A;Molecule type: mRNA
A;Residues: 1-234 cEHR>
A;Cross-references: UNIPARC:UPI0000176F05
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin homology <IMM>
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A.Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C.Superfamily: immunoglobulin C region; immunoglobulin homology C, Keywords: immunoglobulin F;20-85/Domain: immunomical control c
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89.7%; Pred. No. 7.5e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1172; DB 2;
Pred. No. 1.1e-81;
4; Mismatches 6;
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Local Similarity 95.6%;
Les 215; Conservative '
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Best Local Similarity
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A;Contents: Zie
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Judue [1976]

Judue
A;Cross-references: UNIPARC:UPI0000173797

A;Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain A;Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 cd A;Note: the sequence of residues 42-76 was taken from the reference that follows

B;Michaelsen, T.E.; Frangione, B.; Franklin, E.C.

J. Biol. Chem. 252, 883-889, 1977

A;Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication A;Title: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein W A;Accession: A92219
                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 12-97 <MIC>
A;Cross-references: UNIPARC:UPI0000173798
A;Note: the hinge region in gamma-3 chains is about four times as long as in other gamma
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A; Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A; Note: the revised sequence differs from that shown in having 60-Ala and in the amidatic
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A;Gross-references: GDB:119338; OWIM:147110
A;Gross-references: GDB:119338; OWIM:147110
A;Gross-references: GDB:133-14432.33
A;Gross-references: GDB:133-14432.33
A;Map position: 14432.33-144432.33
A;Map position: 14432.33-144432.33
A;Map position: 14632.33-144432.33
A;Map position: 14632.33-144432.33
A;Map position: Immunoglobulin nome of immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-65/Domain: immunoglobulin homology <IM3>
F;23-306/Domain: immunoglobulin homology <IM3>
F;23-306/Domain homology <IM3>
F;23-306/Domain homology <IM3>
F;
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Biochem. J. 121, 217-225, 1971
Biochem. J. 121, 217-225, 1971
A; Title: Disulphide bridges of the heavy chain of human immunoglobulin (A; Feference number: S. MUID:72033500; PMID:4940472
A; Concents: annotation; myeloma protein Sa, disulfide bonds
R; Frangione, B.; Milstein, C.; Pink, J.R.b.
Nature 221, 145-148, 1969
A; Title: Structural studies of immunoglobulin G.
A; Feference number: A93157; MUID:69064124; PMID:5782707
A; Contents: annotation; Sa, disulfide bonds
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A;Molecule type: protein
A;Residues: 238-275 <HOF>
A;Cross-references: UNIPARC:UP10000173794
R;Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A;Reference number: A94591
```

87.9%; Score 1107; DB 1; Length 326;

Query Match

Ig gamma-2 chain C region - human C;Species: Homo sapiens (man)

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Ig gamma chain C region - rabbit (domestic rabbit)
Cispecies: Orycolagus cuniculus (domestic rabbit)
Cjate: 24-Apr-1984 #sequence_revision 15-Nov-1984 #text change 09-Jul-2004
Cjate: 24-Apr-1984 #sequence_revision 15-Nov-1984 #text change 09-Jul-2004
CjAccession: A31749; A90220; A3328; A90245; A94416; A02161
R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
A;Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplot<sup>4</sup>
A;Reference number: A91749; MUID:84030930; PMID:6313520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Cross-references: UNIPROT:PO1870; UNIPARC:UPI000012837D
A,Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr
R;Pratt, D.M.; Mole, L.B.
Biochem. J. 151, 337-349, 1975
A;Title: Sequence studies on the constant region of the Pd sections of rabbit immunoglob<sup>†</sup>
A;Reference number: A90290; MUID:76135469; PMID:1243651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A;Residues: 1-47,'E',49-71,'PV',72-128 <PRA>
A;Cross-references: UNIPARC:UFID0001737AB
Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
A;Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chaiff
A; Reference number: A93928, MUID:83299917; PMID:6193512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; McGecule type: protein
A; Residues: 129-131,155-172,°D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'Q';
A; Residues: 129-131,155-172,'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'Q';
A; Cross-references: UNIPARC: UP100001737Ab; UB5-Ala
A; Note: this has the e15 allotypic marker, 185-Ala
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into ld
C; Superfamily: immunoglobulin cregion; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F; 20-0-27 Domain: immunoglobulin homology < IMI>
E; 236-303/Domain: im
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PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFF 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;173/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                               LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.1%; Score 883; DB 1; 64.5%; Pred. No. 1.3e-59; ive 34; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Matches 160; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-323 < BER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Accession: A94416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A91749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Accession: A90290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: A93928
                                                                                                                                                       191
                                                                                                                                                                                                                               286
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C;Species: Homo sapiems (man)
C;Species: Homo sapiems (man)
C;Species: Homo sapiems (man)
C;Decies: Homo sapiems (man)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C;Date: 02-Apr-1982 #sequence of a human immunoglobulin C-gamma4 gene.
A;Reference number: A90933; WUID: 83157104; PWID: 6299662
A;Accession: A90934
A;Wolecule type: DNA
A;Residues: 1-327 < ELDA
A;Tite: Human immunoglobulin sublclasses: Partial amino acid sequence of the constant of the consta
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                                                                                                                                                                   NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                               ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 ISKTKGOPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
                                                                                                                       1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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                                           Indels
           88.4%; Pred. No. 1.4e-76; ive 12; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 87.1%; Score 1097; DB 1; Best Local Similarity 90.5%; Pred. No. 8.1e-76; Matches 201; Conservative 11; Mismatches 10;
                                                   205; Conservative
           Similarity
                                                                                                                                                                                                   66
                                                                                                                                                                                                                                                                               61
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           Best Local
Matches 20
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gramma 4 chain constant region - pig (fragment)
Cispecies: Sus scrota domestica (domestic pig)
Cispecies: Sus scrota domestica (domestic pig)
Cispecies: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
Ciscossion: 147162
Cispecies: 1: Sun, J.; Butler, J.E.
J. Immunol. 153, 3856-3873, 1994
A.Fitle: Five putative subclasses of swine IgG identified from the cDNA sequences of a significant number: 147169; MUID:95015845; PMID:7930579
A;Reference number: 147162
A;Accession: I47162
A;Accession: I47162
A;Accession: I47162
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-277 ckAC>
A;Coss-references: UNIPARC:UPI0000115527; EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PIT:
Cross-references: UNIPARC:UPI0000115524; EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PIT
                                                                                                                                                                                                                                                                                                                                                                                                                     71 NVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPRE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSVGS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 GVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 VQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig gamma-2 chain C region - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225 PQVYTLPPHABELSRSKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49 TKTKPPCPICPACEGPGPSAFIFPPKPKDTLMISRTPKVTCVVVDVSQENPEVQFSWYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169 GQTREPQVYTLPPPTEELSRSKVTLTCLVTGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 THTCPPCP-APELLG-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
                                                                                                                                                                                                                                                                                                      <u>ب</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 277;
                                          C,Genetics:
A,Gene: 1gG2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
P;133-202/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Gene: IgG4
C,Superfamily: immunoglobulin C region; immunoglobulin homology
F,82-151/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  285 YFLYSKFSVDKASWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328
                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                                                                                                                                                             68.9%; Score 868.5; DB 2;
70.1%; Pred. No. 1.6e-58;
iive 32; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.7%; Score 865; DB 2;
69.0%; Pred. No. 2.5e-58;
iive 32; Mismatches 35
                                                                                                                                                                                                                          Query Match
Best Local Similarity 70.1%
Matches 157; Conservative
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Best Local Similarity 69.01
Matches 158; Conservative
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G2GP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     January 1990 and 20 chain constant region - pig (fragment)
[1] gamma 2b chain constant region - pig (fragment)
[2] Spacies: Sus seroca domestic pig)
[3] Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
[3] Accession: 147160
[4] A. Tille: Five putative subclasses of swine IgG identified from the cDNA sequences of a A. Reference number: 147159; MUID:95015845; PMID:7930579
[5] A. Molecule type: mRNA
[6] A. Molecule type: mRNA
[7] A. Molecule type: mRNA
[
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19 gamma 2a chain constant region - pig (fragment)

19 gamma 2a chain constant region - pig (fragment)

19 gamma 2a chain constant region - pig (fragment)

10 Spaces Sus scrots domestica (domestic pig)

11 Spaces Sus scrots domestica (domestic pig)

12 Spaces Sus scrots Sus, J.; Butler, J.E.

13 Sus, J.; Butler, J.E.

14 N. Racaskovics, I.; Sus, J.; Butler, J.E.

15 Sus, J.; Butler, J.E.

16 A. Racaskovics, I.; Sus, J.; Butler, J.E.

17 A. Races Sus, I.; Sus, J.; Butler, J.E.

18 A. Races Sus, I.; Sus, J.E.

18 A. Races Sus, I.; Sus, J.E.

18 A. Races Sus, J. Races Sus, J.E.

18 A. Races Sus, J. Races 
                                                                                        71 NVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPRE 130
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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llarity 70.1%; Pred. No. 1.6e-58;
Conservative 32; Mismatches 32;
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SISRSPGK 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLSLSPGK 232
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Matches 157;
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C;Accession: 147158
R;Kacskovics, I.; Sun, J.; Butler, J.E.
A; Tmmunol. 153, 3565-3573, 1994
A;Title: Putative subclasses of swine 1gG identified from the cDNA sequences of a 8
A;Reference number: 147158; MUID:95015845; PMID:7930579
A;Accession: 147158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross references: UNIPARC: UPI0000115523; EMBL: U03778; NID: 9433121; PIDN: AAA52216.1; P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 BPQVYTLPPSRDELTKNQVSLTCLVKGPYPSDIAVEWESNGQ--PENNYKTTPPVLDSVG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig gamma 1 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Pomain: immunoglobulin homology <IMM>
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69.3%; Pred. No. 6.4e-57;
tive 30; Mismatches 36
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Best Local Similarity 69.3%,
Matches 156; Conservative
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A; Residues: 1-328 < KAC>
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  C.Accession: A9453; A90352; A90359; A90384; A90385; A02151
A.Accession: A9453; A90325; A90359; A90384; A90385; A02151
A.Accession: A9553
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A.Accession:
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67.4%; Pred. No. 1e-57;
ive 28; Mismatches 42;
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Matches 157; Conservative
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Q6n089
Q5efe5
Q6gmw7
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Q6pj£1
Q6n096
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GenCore version 5.1.6
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2: uniprot_trembl:*
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Q8nf17 homo sapien													
Q8NF17_HUMAN	IGHG2 HUMAN	Q6N093 HUMAN	Q6MZU6_HUMAN	Q6P6C4 HUMAN	IGHG4 HUMAN	QSTC63 HUMAN	Q68CN4 HUMAN	Q6MZX7_HUMAN	GC RABIT	Q95M34 HORSE	IGHG2 CAVPO	GCB RAT	Q5M839_RAT
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Ponsting! H., Hilschmann N.,
"The rule of antibody structure. The primary structure of a monoclonal
Igg1 immunoglobulin (myeloma protein Nie). III. The chymotryptic
peptides of the H-chain, alignment of the tryptic peptides and
discussion of the complete structure.",
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN SEQUENCE OF 1-135 (MYELONA PROTEIN EU).
MEDLINE=71064024; PubMed=5489771;
Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
Waxdall M.J., Bdelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
Biochemistry 9:3161-3170(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7."; Biochemistry 9:3171-3181(1970).
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Schnidt W. E., Jung H.-D., Palm W., Hilschmann N.;
Three-dimensional structure determination of antibodies. Primary
structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
IsULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN SEQUENCE OF 136-329 (EU).
MEDLINE-71064025; PubMed-5530842;
Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [5] PROTEIN SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Ig gamma-1 chain C region.
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PROTEIN SEQUENCE (MYELOMA PROTEIN NIE).
MEDLINE=77070269; Pubmed=826475;
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                                               PRT;
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MEDLINE=82274238; PubMed=6287432;
                                               STANDARD;
                                                                                                                                                                                                                                                                        Name=IGHG1;
Homo sapiens (Human)
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K -> R (in GlM(3) marker).
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D -> E (in GlM(non-1) marker).
/FIId=VAR 003887.
L -> M (in GlM(non-1) marker).
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                                                N-linked (GlcNAc. . .)
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Matches 225; Conservative
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                                                                                                                                                                                                                                  RY NEDLINE-81208100; PubMed=7236608;
RX MEDLINE-81208100; PubMed=7236608;
RA Defisenhofer J.;
RA Defisenhofer J.;
RY and its complex with fragment and atomic models of a human Pc fragment
RT and its complex with fragment B of protein A from Staphylococcus
RT anceus at 2.9- and 2.8-A resolution.";
Blochemistry 20:2361-2370 (1981) allotypic marker, 97-K, and the
CC GIM(1) markers, 239-D and 241-L. KOL and EU sequences have the
GIM(3) marker and the GIM (non-1) markers.
CC GIM(3) marker and the GIM (non-1) markers
CC -1- MISCELLANEOUS: Nie also differs in the amidation states of 35,
CC -1- MISCELLANEOUS: EU also differs in the amidation states of residues
CC -1- MISCELLANEOUS: 198, 269 and 272 and in the order of residues
CC -258-272.
                                                                                                          MEDLINE=77070267; PubMed=1002129;
Dreker L., Schwarz J., Reichel W., Hilschmann N.;
Dreker L., Schwarz J., Reichel W., Hilschmann N.;
Inte of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myelone in Nie), I: purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";
Mpppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MISCELLANEOUS: KOL also differs in the amidation states of residues 198, 267 and 272.
             Gall W.E., Edelman G.M., "The covalent structure of a human gamma G-immunoglobulin. X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3D-structure; Direct protein sequencing; Glycoprotein; Immunoglobulin C region; Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, J00228; AAC82527.1; ALT_INIT; Genomic_DNA.
PNB, J49433; GHHU.
PDB; J477; X-ray; H=1-103.
PDB; JDA7; X-ray; H=1-101.
PDB; JDS1; X-ray; AB=120-136.
PDB; JFC2; X-ray; AB=106-329.
PDB; JFC2; X-ray; AB=106-329.
PDB; JFC2; X-ray; BD=16-329.
PDB; JTS1; X-ray; AB=107-330.
PDB; JTS1; X-ray; AB=107-330.
PDB; JTS1; X-ray; AB=107-330.
PDB; JTS1; X-ray; AB=107-330.
PDB; JTS2; X-ray; AB=107-330.
PDB; JTS3; X-ray;
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InterPro; IPR003597; Ig c1.
InterPro; IPR003597; Ig c1.
Pfam; PF07654; C1-set; 3.
PROSITE; PS00230; IG MHC; 2.
3D-structure; Direct protein sequencing;
MEDLINE=71064027; PubMed=4923144;
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                                              Intrachain disulfide bonds.";
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X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Altschul S.F., Zeeberg B.B., Buctow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B.B., Buctow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,

A Batchento M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.A., McEwan P.J., McKernan K.J., Male M.A., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rachy J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shewchenko Y., Bouffard G.G.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Reference A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                      NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                   US-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Mypothetical protein.
Hypothetical protein.
Hypothetical Hybotherin.
Bukaryota; Merann.
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GO; GO:0016021; C:integral to membrane; IEA.
InterPro; IPR001559; IG.
InterPro; IPR00110; IG-1ike.
InterPro; IPR003096; IG-0;
InterPro; IPR00409; IG-0;
INTERPO; IRR00409; IG-0;
INTERPO; IRR00406; IG-0;
IRR00406; IG-0;
IRR00406; IG-0;
IRR00406; IG-0;
IRRD0406; IRRD0406; IG-0;
IRRD0406; IR
                                                                                                                                                                                                                                                                                                                                                                                                                QGGMX6_HUMAN PRELIMINARY;
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SEQUENCE 465 AA, 5
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MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MISCALL, Felingold E.A., Grouse L.H., Derge J.G.,

Altachni S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschni S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Diatchenko L., Marusina K., Perers G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Murny D.M., Sodergren E.J., Lu X., Glabs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimmood J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimmood J.W., Schmutz J., Mysrs R.M.,

Schnertion and initial analysis of more than 15,000 full-length human
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                                                                                                                                       Gaps
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Length 465;
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
Score 1225; DB 2;
Pred. No. 9.1e-90;
3; Mismatches 4;
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TISSUE=Peripheral Nervous System;
              97.2%;
97.0%;
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Q6IN78;
              Query Match
Best Local Similarity 97.00
Matches 225; Conservative
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Name=IGHG1;
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Query Match
Best Local Similarity 97.0°
Matches 225; Conservative
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01-OCT-2003 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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Name=IGHG1;
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Chuler G.D.,
Riausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F.,
Batchenko D., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A. Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield A.S., Soner B. W., Marra M.A.,
Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Pred. No. 9.1e-90;
3; Mismatches 4; Indels C
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Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BC092518; AAH92518.1; -; mRNA.
SEQUENCE 469 AA; 51254 MW; AC13448E3047784F CRC64;
SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 3.
SMART; SM00406; IGv; 1.
PROSITE; PSS0035; IG LIKE; 4.
PROSITE; PSS00290; IG MHC; UNKNOWN 2.
SEQUENCE 466 AA; 50854 MW; 53EBOBCEDE81076E CRC64;
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Last annotation update)
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                                                                                                                                                                     97.2%;
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Matches 225, Conservative
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**X. Table=5918825; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Seinger D.H., Schaefer C.F., Bhat N.K., A Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., More T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Romnstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Anderson D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Halton B.K., Ketreman M., Rodar A., Rodrigues S., Sanchez A., Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield T.S.N., Krzywinski M.I., Skalska U., Smailus D.E., T. Galencation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                             61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
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                                                                                  Gaps
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       Length 469;
                                                                           4; Indels
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Last annotation update)
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Score 1225; DB 2;
Pred. No. 9.2e-90;
3; Mismatches 4;
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InterPro; IPR003597; Ig_C1.
InterPro; IPR003065; Ig_MHC.
InterPro; IPR0035965, Ig_W.
Pfam; PP07654; C1-8et; 3.
97.2%;
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Q7Z7P5;
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Name=IGHG1;
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A Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toobhyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunatane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rachesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Marra M.A.;

Generation and initial analysis of more than 15,000 full-length human
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                     NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                 Gaps
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                                                                                                                                    97.2%; Score 1225; DB 2; Length 469; 97.0%; Pred. No. 9.2e-90;
                                                                                                                                                                              4; Indels
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Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC053984; AAH53984.1; -; mENA.
HSSP; P01857; IHZII. T. 1186
                                                                                         C8D5BE12BAAF795C CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
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                                                                                                                                                       97.0%; Pred. No. 9.2e tive 3; Mismatches
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                    Immunoglobulin domain.
SEQUENCE 469 AA; 51395 MW;
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InterPro; IPR003597; Ig_c1.
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Q7Z5W1;
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TISSUE=Spleen;
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MEDLINE-22388257; PubMed-1247932; DOI=10.1073/pnas.242603899;
MEDLINE-22388257; PubMed-1247932; DOI=10.1073/pnas.242603899;
A Klausher R.D., Collins F.S., Wagner L.H., Derge J.G.,
A Klausher R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Diatchenko L., Marusha K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusha K., Farmer A.A., Rubin G.M., Hong L.,
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A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
A Robert S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley D.M., Sodergren R.J., Lu X., Gibbs R.A.,
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A Hilalon D.X., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Willalon D.X., Muzny D.M., Shevchenko Y., Boulfard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Blakesley R.W., Touchman J.W., Schein J.B., Marra M.A.;
A Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
A Generation and initial analysis of more than 15,000 full-length human
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                          Length 470;
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                        InterPro; IPR03596; 1g~v.
Pfam; PF07654; C1-set; 3.
SMART; SM04065; IC4; 1.
PROSITE; PS50835; IG_LIKE; 4.
Hypothetical protein; Immunoglobulin domain.
SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                      Ouery Match 97.2%; Score 1225; DB 2; Best Local Similarity 97.0%; Pred. No. 9.2e-90; Matches 225; Conservative 3; Mismatches 4;
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InterPro; IPR003006; Ig_MHC.
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NUCLEOTIDE SEQUENCE.
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Query Match
Best Local Similarity 97.0°
Matches 225; Conservative
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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A wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,

Pobo G., Han M., Wilemann S.;

Loudhitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.

EMBL; BX640627; CAE45781.1; -; mRNA.

HSSP; P01861; IADO.

InterPro; IPR003109; Ig.

InterPro; IPR003109; Ig.

InterPro; IPR003597; Ig.

InterPro; IPR003597; Ig.

InterPro; IPR003596; Ig.

InterPro; IPR00406; Ig.

InterPro; IPR0406; IG.

InterPro; IRR SM0406; IG.

IRR SM040
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                                                                       InterPro; IPR00110; Ig-like.
InterPro; IPR003109; Ig-like.
InterPro; IPR003306; Ig-like.
InterPro; IPR003306; Ig-d.
InterPro; IPR003596; Ig-d.
InterPro; IPR00409; Ig-d.
InterPro; IPR00409; Ig-d.
InterPro; IPR00409; Ig-d.
InterPro; IPR00409; Ig-d.
InterPro; IPR00407; Ig-d.
InterPro; IPR00407; Ig-d.
InterPro; IPR00407; Ig-d.
InterPro; IPR00407; Ig-d.
InterPro; IPR09407; Ig-d.
INTERPRO; IRR09407; IRR09407; IG-d.
INTERPRO; IRR09407; IRR0940
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686F15220.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 97.2%; Score 1225; DB 2; Best Local Similarity 97.0%; Pred. No. 9.2e-90; Matches 225; Conservative 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     472 AA
EMBL; BC018747; AAH18747.1; -; mRNA.
HSSP; P01861; 1ADQ.
SMR; Q6PJA4; 20-470.
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Q6N089;
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                                                                                                                                                 241 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 300
                                                                                                                                                                                                                                 61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                 301 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 360
                                                                                                                                                                                                                                                                                                                                                  121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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A Gaucher C., Klein P., Bellard R.;
Gaucher C., Klein P., Bellard R.;
The Sequence determination of the recombinant human anti-RhD moncart artibody T125.";
L Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
R EMBL, AY894992; AAW82028.1; -; mRNA.
R InterPro; IPR003599; Ig.-1;
R InterPro; IPR003599; Ig.-1;
R InterPro; IPR003597; Ig.-1;
R InterPro; IPR003596; Ig.-1;
R InterPro; IPR003596; Ig.-1;
R Ffam; PF07654; C1-set; 3.
R SMART; SM00409; IG; 2.
R SMART; SM00409; IG; 2.
R SMART; SM00409; IGC; 3.
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llarity 97.0%; Pred. No. 9.3e-90;
Conservative 3; Mismatches 4; Indels
Length 472
                                                           4; Indels
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Anti-RhD monoclonal T125 gammal heavy chain precursor.
Homo sapiens (Human).
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475 AA; 52362 MW; 1367D400DC7D2859 CRC64;
Score 1225; DB 2;
Pred. No. 9.2e-90;
3; Mismatches 4;
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PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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     97.2%;
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QSEFES;
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NUCLEOTIDE SEQUENCE.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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                                                    PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                         PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 475
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Pred. No. 9.3e-90;
3; Mismatches 4; Indels
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073782; AAH73782.1; -; mRNA.
GO; GO:0016021; C:integral to membrane; IEA.
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                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Hypothetical protein.
                                                                                                                                                                            PRT;
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InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
InterPro; IPR003596; Ig_V.
Pfam; PR07654; Cl.set; 3.
SWART; SW00407; IGcl; 3.
SWART; SW00407; IGcl; 3.
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97.0%;
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Best Local Similarity 97.0%
Matches 225; Conservative
                                                                                                                                                                          OGGMW7_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                             Hypothetical protein.
Homo sapiens (Human).
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RA Aleushers R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D., Riusner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D., Alteshul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhar N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Brownstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.E., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Rohards S.A., McKernan K.J., Malk J.J., Hulyk S.W., R., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Antilan M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Sheken B.D., Dickson M.C., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., And Mannan and initial analysis of more than 15,000 full-length human
120
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                             NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                           121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLICLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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InterPro; IPR003599; 19.
InterPro; IPR003109; 19.
InterPro; IPR003109; 19.
InterPro; IPR003109; 19.
InterPro; IPR003006; 10.
InterPro; IPR00409; 10.
InterPro; IPR00409; 10.
IPR0011E; PS00409; 10.
IPR0011E; PS00409; 10.
IPR0511E; PS00409; 10.

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Homo sapiens (Human).
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05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
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Q6P055;
                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 97.0
Matches 225; Conservative
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05-JUL-2004 (TrEMBLrel.
Hypothetical protein.
Homo sapiens (Human).
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                        305 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                  EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                              NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                    ISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP
                                                                       1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                          Gaps
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                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hu Z., Garen A., Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases. EMBL, AF272774; AAK58686.2; -; MRNA. HSSP; P08709; IKLI.
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SNR; JOSEPOB. 39-180, 191-444, 447-679.

Ensembl; ENSGO000057593; Home sapiens.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0004263; F:calcium ion binding; IEA.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004269; F:crypsin activity; IEA.
GO; GO:000508; P:proteolysis and peptidolysis; IEA.
INTERPRO; IPRO00152; Asx. hydroxyl_S.
INTERPRO; IPRO01841; EGF_Ca.
INTERPRO; IPRO01841; EGF_Ca.
INTERPRO; IPRO01841; EGF_IA.
INTERPRO; IPRO01891; EGF_IA.
INTERPRO; IPRO01894; PEPTIGASE_SIA.
INTERPRO; IPRO01894; PEPTIGASE_SIA.
INTERPRO; IPRO01894; PEPTIGASE_SIA.
INTERPRO; IPRO01894; VIUK. dep_GIA.
INTERPRO; IPRO01894; PEPTIGASE_SIA.
INTERPRO; IPRO01894; VIUK. dep_GIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q96PQ8 HUMAN PRELIMINARY; PRT; 679 AA.
Q96PQ8;
Q91-DEC-2001 (TrEMBLrel. 19, Created)
O1-JUN-2003 (TrEMBLrel. 24, Last sequence update)
O1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Factor VII active site mutant immunoconjugate.
  Pred. No. 9.3e-90;
                          3; Mismatches
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PRINTS; PRO0001; EGPBLOOD.
PRINTS; PRO0001; GLABLOOD.
SWART; SM00179; EGF_CA; I.
97.08;
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                       Matches 225; Conservative
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Pfam; PF00008; EGF; 1.
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Best Local Similarity
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TISSUE-Peripheral Nervous System;

KX MEDLINE-22380257; PubMed-12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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RA Didtchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Portage M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

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Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

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Rabaciguez A.C., Grimmood J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Ratharfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rechnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Last annotation update)
SWART; SMO0407; IGG1; 1.

SWART; SMO0100; ITYP, SPC; 1.

PROSITE; PS001010; ASZ, HYDROXYL; UNKNOWN_1.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS01187; EGF_A; 1.

PROSITE; PS01187; EGF_A; 1.

PROSITE; PS0198; GLA_1; UNKNOWN_1.

PROSITE; PS05098; GLA_2; 1.

PROSITE; PS05098; IG_IKE; 2.

PROSITE; PS05099; IG_IKE; 2.

PROSITE; PS05099; IG_IKE; 1.
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Pfam; PF07654; C1-set; 3.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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THE German CDNA Consortium;
The German CDNA Consortium;
Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
Han M., Wiemann S.;
Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
EMBL, BSK40047; CAE45972.1; -; mRNA.
HSSP; PO1861; JADO.
SWR; Q6MZQ6; 20-475.
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                                              NUCLEARLY SECURED.

Strausberg R.;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (UAN-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (UAN-2004) to the EMBL/GenBank/DDBJ databases.
HSSP; PO1861; 1ADQ.
InterPro; IPR001599; Ig.
InterPro; IPR00110; Ig-like.
InterPro; IPR00110; Ig-like.
InterPro; IPR001597; Ig_c1.
InterPro; IPR001596; Ig_v.
InterPro; IPR001596; Ig_v.
InterPro; IPR001596; Ig_v.
InterPro; IPR001596; Ig_v.
INTERPRO; SM00409; IG; 2.
SWART; SM00409; IG; 2.
SWART; SM00409; IG; 2.
SWART; SM00409; IG; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_LIKE; UNKNOWN_2.
                                                                                                                                                                                                                                                                    473 AA; 51344 MW; 9816D56A77129B57 CRC64;
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and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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InterPro; IPR007110; IG-11ke.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                       NUCLEOTIDE SEQUENCE.
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NCBI_TaxID=9606;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                        364 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
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THE German cDNA Consortium;

Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,

Fobo G., Han M., Wiemann S.;

Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.

EMBL; BX640622; CAE45776.1; -; mRNA.

HSSP; P01861; IADO.
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96.6%; Pred. No. 2e-89;
ive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                         5; Indels
SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 3.
SMART; SM00407; IGc1; 3.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 480 AA; 52612 MW; 225247F3D35AEC18 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686001196.
                                                                                                                                                                                                    96.9%; Score 1221; DB 2;
ilarity 96.6%; Pred. No. 1.9e-89;
Conservative 3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001359; IG.
InterPro; IPR00110; IG-like.
InterPro; IPR007110; IG-like.
InterPro; IPR003597; IG_1.
InterPro; IPR003597; IG_1.
InterPro; IPR003596; IG WHC.
InterPro; IPR003596; IG WHC.
InterPro; IPR003596; IG WHC.
InterPro; IPR00409; IG, 2.
SWART; SW00409; IG, 2.
SWART; SW00406; IGV; 1.
PR0SITE; PS002590; IG_LKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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Q6N094;
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NUCLEOTIDE SEQUENCE.
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Best Local Similarity
Matches 224; Conserv
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249 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 308
                              8 6 8 6 8
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Search completed: November 30, 2005, 00:56:31 Job time: 128.768 secs

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US-08-595-043A-50
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                                                        November 30, 2005, 00:51:35; Search time 27.7391 Seconds (without alignments) 691.469 Million cell updates/sec
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                                                                                          US-09-847-208B-3
1260
1 EPKSCDKTHTCPPCPAPELL......MHEALHNHYQQRSLSLSPGK 232
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: /cgn2 6/ptodata1/jaa/6_COMB.pep:*
: /cgn2 6/ptodata1/jaa/H_COMB.pep:*
: /cgn2 6/ptodata1/jaa/H_COMB.pep:*
: /cgn2 6/ptodata1/jaa/PGTUS_COMB.pep:*
: /cgn2 6/ptodata1/jaa/RE_COMB.pep:*
: /cgn2 6/ptodata1/jaa/Re
         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-968-362A-26
US-09-178-869-2
US-09-178-869-2
US-09-180-100-11
US-09-949-713-11
US-08-236-311-7
US-09-180-100-22
US-09-180-100-22
US-09-949-713-22
US-09-180-100-22
US-09-999-99
US-09-176-228-3
US-09-176-228-3
PCT-US95-03866-12
PCT-US95-03866-12
PCT-US95-03866-12
US-08-478-888A-7
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length
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Maximum DB seq
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NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
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12, Appli.
12, Appli.
14, Appli.
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12, Appli.
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CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OOPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/595,043A
FILING DATE: 31-JAN-1996
CLASSIFICATION NUMBER: 31-JAN-1996
ATTOMEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET UNMBER: SGAR-00371
TELEFONNE: (415) 705-8410
TELEFONNE: (415) 705-8410
TELEFAN: (415) 705-836
INFORMATION FOR SEQ ID NO: 50: SEQUENCE CHARACTERISTICS:
LEMOTH: 232 amino acids
TYPE: amino acids
TYPE: Allocat
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Pred. No. 3.5e-116;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                  PATENT NO. 5935824
GENERAL INFORMATION:
APPLICANT: SGARLATO, GREGORY D.
TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
INDMER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                   US-08-48-550-12
US-09-526-098-4
US-09-526-098-12
US-09-383-916-4
US-09-383-916-12
US-09-758-173-4
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US-09-576-424-4
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-08-378-939-10
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97.0%;
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Best Local Similarity 97.0
Matches 225; Conservative
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61 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
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APPLICANT: Tao, Weng
APPLICANT: Tao, Weng
APPLICANT: Wong, Shou
APPLICANT: Hickey, William F
APPLICANT: Hickey, William F
APPLICANT: Bactege, B. Edward
TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
FILE REFERENCE: 1781-043
CURRENT FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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Score 1225; DB 2;
Pred. No. 3.5e-116;
3; Mismatches 4;
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Pred. No. 5.9e-116;
3; Mismatches 4;
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APPLICANT: Tao, Weng APPLICANT: Wong, Shou
      97.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tch 97.2%; al Similarity 97.0%; 225; Conservative
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   Query Match
Best Local Similarity 97.04
Matches 225; Conservative
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ORGANISM: Homo sapiens
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US-09-761-413-2
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Best Local S:
Matches 225
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                                                                                                                                                                                                                                                                                                                             Sequence 26, Application US/09968362A
Patent No. 6797493
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sun, Bill
APPLICANT: Sun, Cecily R
APPLICANT Sun, Ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
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                                               61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
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Fatent No. 6900292
GENERAL INFORMATION:
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Cecily R
ITILE OF INVENTION: Increased biological
ITILE OF INVENTION: activities
ITILE OF INVENTION: activities
FILE REFERENCE: 028UN2001
CURRENT APPLICATION NUMBER: US/09/932,812A
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3:1
SED ID NOS: 26
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                                                                                                                                                                                                                                                                                RESULT 2
US-09-968-362A-26
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US-09-932-812A-26
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181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/2.
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Best Local Similarity 97.0<sup>§</sup>
Matches 225; Conservative
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CRGANISM: Homo sapiens
US-09-949-713-11
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                                                                                                                                                           US-09-949-713-11
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US-08-236-311-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTYLHQDWLNGKEYKCKVSNKALFAPIEKT 219
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APPLICANT: Hammang, Joseph P.
APPLICANT: Baetge, E. Edward
TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
FILE REFERENCE: 17810-043
CURRENT APPLICATION NUMBER: US/09/761,413
CURRENT FILING DATE: 2001-01-16
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                        97.2%; Score 1225; DB 2; Length 331; 97.0%; Pred. No. 5.9e-116;
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; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NACAMURA, No. 6306395io
; APPLICANT: NACAMURA, No. 6306395io
; TILLE OF INVENTION: NOVEL FAS ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/180,100
; CURRENT FILING DATE: 1998-11-02
; EARLIER FILING DATE: 1998-11-02
; EARLIER FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PATENTIN Ver. 2.0
; SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
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Best Local Similarity 97.03
Matches 225; Conservative
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Best Local Similarity 97.0
Matches 225; Conservative
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US-09-180-100-11
                                                                                                                                                                                                                                                           LENGTH: 331
TYPE: PRT
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189 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
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309 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHBALHNHYTQKSLSLSPGK 360
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                                                                                                                     ; Sequence 11, Application US/09949713; Patent No. 6953847; Patent No. 6953847; GENERAL INFORMATION: APPLICANT: NAKAWURA, No. 6953847io APPLICANT: NAKAWURA, Shigekazu TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE; FILLE REFERENCE: 1110-207P; CURRENT FAPLICATION NUMBER: US/09/180,100; PRIOR FILLING DATE: 1998-11-02; PRIOR FILLING DATE: 1998-11-02; PRIOR FILLING DATE: 1997-05-01; NUMBER: OF SEQ. ID NOS: 25; SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97.2%; Score 1225; DB 2;
97.0%; Pred. No. 6.6e-116;
tive. 3; Mismatches 4;
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Fatent No. 5565335
GENERAL INFORMATION:
APPLICANT: Capon, Daniel J.
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Addresson Variants
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSES: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
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Pred. No. 6.9e-116;
3; Mismatches 4;
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COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Generated)

CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/457,918
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Patent No. 6117655
GENERAL INFORMATION:
APPLICANT: Capon, Daniel J.
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/84277
FILING DATE: 18-FEB-1992
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/104329
FILING DATE: 02-OCT-1987
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 444PIC2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 97.0%;
Matches 225; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-08-236-311-7
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US-08-457-918-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 BPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 97.2%; Score 1225; DB 2; Length 371; Best Local Similarity 97.0%; Pred. No. 6.9e-116; Matches 225; Conservative 3; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
STREET: 460 Point San Bruno Blvd
CTTY: South San Francisco
STATE: California
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Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36,575
RR: P0444P1C3
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
FILING DATE: 08/236311
FILING DATE: 0.8M21994

PRIOR APPLICATION NUMBER: 07/936190
FILING DATE: 28-AUG-1992

PRIOR APPLICATION NUMBER: 07/936190
FILING DATE: 28-AUG-1992

PRIOR APPLICATION DATA: 18-PEB-1992

PRIOR APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992

PRIOR APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988

PRIOR APPLICATION NUMBER: 07/250785
FILING DATE: 02-OCT-1987

ATTORNEY/AGENT INFORMATION:
NAME: 07/05/07/104329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/10157408
Patent No. 6710169
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERNCE/DOCKET NUMBER: P04.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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amino acid
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97.2%;
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Best Local Similarity 97.0
Matches 225; Conservative
                                                      Query Match
Best Local Similarity 97.0
Matches 225; Conservative
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CORGANISM: Homo sapiens
US-09-949-713-22
ORGANISM: Homo sapiens
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US-09-949-713-22
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US-10-679-999-9
        US-09-180-100-22
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; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NARAWURA, No. 630639510
; APPLICANT: NARAWURA, No. 630639510
; APPLICANT: NARAWURA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; CURRENT APPLICATION NUMBER: US/09/180,100
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: PCT/JP97/01502
; EARLIER PELLING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver: 2.0
; SQD ID NO 22
; LENGTH: 376
; TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 97.2%; Score 1225; DB 2; Best Local Similarity 97.0%; Pred. No. 6.9e-116; Matches 225; Conservative 3; Mismatches 4;
                                                                                                           APPLICATION DAIRS: US/08/457,918
FILING DATE: 1-UN-195
APPLICATION NUMBER: 08/236311
FILING DATE: 02-WAY-1994
APPLICATION NUMBER: 07/936190
FILING DATE: 26-MG-1992
APPLICATION NUMBER: 07/84277
FILING DATE: 26-MG-1992
APPLICATION NUMBER: 07/250785
FILING DATE: 18-FEB-1988
APPLICATION NUMBER: 07/104329
FILING DATE: 28-SEP-1988
APPLICATION NUMBER: 07/104329
FILING DATE: 02-OCT-1987
                                                                                                                                                                                                                                                                                                                                                                     NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REPERENCE/DOCKET NUMBER: P0444PIC3
TELECOMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
TELEPAX: 415/952-981
TELERX: 910/371-7168
                                      APPLICATION NUMBER: US/10/157,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-157-408-7
  SOFTWARE: patin (Genentech)
                                                        FILING DATE: 28-May-2002
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS
                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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US-09-180-100-22
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205 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 264
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                                                                                                                145 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                                                                         1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPBVKF
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Length 376;
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                                            Indels
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GENERAL INCORMATION:
APPLICANT: NACAMURA, No. 6953847io
APPLICANT: NACAMURA, Shigekazu
TITIE OF INVENTION: NOVEL FAB ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P
CURRENT APPLICATION NUMBER: US/09/180,100
PRIOR APPLICATION NUMBER: US/09/180,100
PRIOR APPLICATION NUMBER: PCT/JP97/01502
PRIOR APPLICATION NUMBER: PCT/JP97/01502
PRIOR FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1225; DB 2;
Pred. No. 7.1e-116;
3; Mismatches 4;
  Score 1225; DB 2;
Pred. No. 7.1e-116;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Sequence 22, Application US/09949713
; Patent No. 6953847
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Patent No. 6936439
GENERAL INFORMATION:
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97.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 61
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APPLICANT: Mann, Michael B.
Hecht, Randy I.
TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: /note= "Met (ATG) starts at SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                          COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM C compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1225; DB 2;
Pred. No. 7.1e-116;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/679,999
FILING DATE: 06-Oct-2003
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: US/09/68,528
FILING DATE: 09-May-2000
APPLICATION NUMBER: 09/267,517
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Knight, Matthew W.
REGISTRATION NUMBER: 36,846
INFORMATION FOR SEQ ID NO: 9:
                                                                                NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: Amgen Inc.
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 379 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 97.0%;
Matches 225; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
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Sequence 3, Application US/08784512
Patent No. 5872209
GENERAL INFORMATION:
APPLICANT: BARTNIK, Eckart
APPLICANT: BIDENMUBLLER, Bernd
APPLICANT: BUETTNER, Frank

RESULT 14 US-08-784-512-3

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TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)

TITLE OF INVENTION: and native aggrecan to study the proteolytic activity of TITLE OF INVENTION: "Aggrecanase" in cell culture systems

TORRESPONDENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSE: FOLGY & Lardner
STREET: Suite 500, 3000 K Street, N.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
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                                                                                                                                                                                                                          CUUTIX: WASHINGLOW, D.C.
CUUTIX: WASHINGLOW, D.C.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,512
FILING DATE: 17-DAN-1997
FILING DATE: 18-DAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, PATITICA D.
REGISTRATION NUMBER: 33,683
REFERENCE/POCKET NUMBER: 33,683
REFERENCE/POCKET NUMBER: 18748/311
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELEFRAX: (202)672-5300
TELEFRAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 97.2%; Score 1225; DB 1; Best Local Similarity 97.0%; Pred. No. 7.6e-116; Matches 225; Conservative 3; Mismatches 4;
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; Sequence 3, Application US/09176228
; Patent No. 6180334
; GENERAL INFORMATION:
APPLICANT: BARTNIK, Eckart
APPLICANT: BIDETHNER, Bernd
APPLICANT: GIDETHNER, Frank
APPLICANT: CATERSON, Bruce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Protein
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US-08-784-512-3
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us-09-847-208b-3.rai

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TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
TITLE OF INVENTION: And native aggrecan to study the proteolytic activity of
TITLE OF INVENTION: "Aggrecanase" in cell culture systems
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLDY & Lardner
STRET: Suite 500, 3000 K Street, N.W.
CITY: Washington, D.C.
ZID: COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PATENTIN BATA:
APPLICATION NUMBER: US/09/176,228
FILING DATE:
PRIOR APPLICATION NUMBER: US/08/784,512
FILING DATE: 11-7-AN-1997
APPLICATION NUMBER: EP 96100682.2
FILING DATE: 18-JAN-1996
ATTONEY/AGENT INPORMATION:
NAME: GRANADOS, PATENTIN 33,683
REFERENCE/DOCKET NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/311
TELEPRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/311
TELEPRATION NUMBER: 2020,672-5309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (204/c...
TELEFAX: 904136
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
"WATH: 396 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Protein
; LOCATION: 1..396
US-09-176-228-3
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Search completed: November 30, 2005, 01:12:51 Job time : 28.7391 secs

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US-10-000-439-3
) Sequence 3, Application US/10000439
; Publication No. US20030064063A1
; GENERAL INFORWATION:
APPLICANT: BAXOn, Andrew
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
; TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-847-208-3
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10, Appl
1, Appli
7, Appli
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                                                                                                                                            November 30, 2005, 00:56:45; Search time 97.087 Seconds (without alignments) 998.449 Million cell updates/sec
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1 EPKSCDKTHTCPPCPAPELL......MHEALHNHYQQRSLSLSPGK
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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(c) 1993 - 2005 Compugen Ltd.
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US-09-389-782-11

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US-10-800-449-26

US-10-800-449-26

US-11-016-518A-26

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US-11-016-518A-26

US-11-016-518A-26

US-10-627-556-684

US-10-627-556-208

US-10-734-661A-6

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US-10-152-363A-6
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Maximum Match 100%
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US-11-128-709-14
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US-10-789-380-37
US-09-995-898A-15
US-09-895-898A-15
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US-10-269-805-68
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US-10-383-902A-6
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US-10-112-582-1
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ALIGNMENTS

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121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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Sequence 3. Application US/09847208
; Publication No. US20030082190A1
; GENERAL INPORMATION:
    APPLICANT: Zaxon, Andrew
    APPLICANT: Zaxon, Andrew
    APPLICANT: Zaxon, Andrew
    APPLICANT: Zaxon, Re
    APPLICANT: Zaxon, Re
    APPLICANT: Zaxon, Redrew
    APPLICANT: Zaxon, Redrew
    APPLICANT: Zaxon, No.
    TITLE OF INVENTION: FURSION MOLECULES AND TREATMENT OF
    TITLE OF INVENTION: FURSION MOLECULES
    TITLE M
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ORGANISM: Homo sapiens
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61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
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OTHER INFORMATION: Fusion between hinge-CH2-CH3 (IgG1) to CH2-CH3-CH4
OTHER INFORMATION: (IgE)
US-09-847-208-7
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279 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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                                                                                                                            Sequence 2, Application US/10000439
Publication No. US20030064063A1
GENERAL INFORMATION:
APPLICANT: SAXON, Andrew
TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES
FILE REPERBURCE: UC067.004A
CURRENT APPLICATION NUMBER: US,10/000,439
CURRENT APPLICATION NUMBER: US 09/847,208
PRIOR FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20030082190A1

GENERAL INFORMATION:
APPLICANT: Saxon, Andrew
APPLICANT: Zhang, Ke
APPLICANT: Zhang, Ke
APPLICANT: Zhu, Daocheng
TITLE OF INVENTION: IgE-MEDIATED ALLERGIC DISEASES
FILE REFERENCE: UC67.002A
CURRENT APPLICATION NUMBER: US/09/847,208
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 177
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.0%; Pred. No. 1.7e-92;
Matches 232; Conservative 0; Mismatches 0;
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ORGANISM: Homo sapiens
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Publication No US20030082190A1
GENERAL INFORMATION:
GURRENT APPLICATION NUMBER: US/09/847,208
GURRENT FILING DATE: 2001-05-01
                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1260; DB 4; 100.0%; Pred. No. 1.1e-92;
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0
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                  CURRENT APPLICATION NUMBER: US/10/000,439
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: US 09/847,208
PRIOR DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 232; Conservative
FILE REFERENCE: UC067.004A
                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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LENGTH: 232
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LENGTH: 330
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US-09-847-208-2
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; Sequence 10, Application US/0996357
; Patent No. US20020133001A1
; GENERAL INFORMATION:
APPLICANT: Gefter, Malcolm L
APPLICANT: Joyal John L
; APPLICANT: Gosselin, Michael
TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE T
TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE T
TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE T
TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE T
FILE REFERENCE: PPI-105
CURRENT APPLICATION NUMBER: US/09/996,357
CURRENT FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-29
PRIOR FILING DATE: 2000-11-29
PRIOR FILING DATE: 2000-11-29
PRIOR FILING DATE: 2000-11-29
PRIOR PLING DATE: 2000-11-29
SEQUENCE OF SEQUE
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Pred. No. 7.1e-90;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                       97.5%; Score 1228; DB 5;
97.4%; Pred. No. 6.1e-90;
iive 2; Mismatches 4;
PRIOR PRIJECATION NUMBER: US 60/562,627
PRIOR FILING DATE: 2004-04-14
PRIOR PPLICATION NUMBER: US 60/511,687
PRIOR PILING DATE: 2003-10-15
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patentin version 3.2
LENGTH: 330
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Best Local Similarity 97.0%;
Matches 225; Conservative
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Best Local Similarity 97.4<sup>†</sup>
Matches 226; Conservative
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US-10-966-673-29
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Publication No. US20050226864A1
GENERAL INFORMATION:
APPLICANT: Protein Design Labs, Inc.
APPLICANT: Hinton, Paul R
APPLICANT: Tsurushita, Naoya
TITLE OF INVENTION: Alteration of Fo-Fusion Protein Serum Half-Lives By Mutagenesis
FILE REPERENCE: 05882.0039.NUNDS07
CURRENT APPLICATION NUMBER: US/10/966,673
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                              EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                             NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
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Publication No. US2003006406341;
GENERAL INFORMATION:
APPLICANT: SAZON, Andrew;
TITLE OF INVENTION: PUSION WOLECULES AND METHODS FOR;
TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES;
FILE REFERENCE: UC67.0044
; CURRENT APPLICATION NUMBER: US/10/000,439;
CURRENT FILING DATE: 2001-10-24;
PRIOR APPLICATION NUMBER: US 09/847,208;
PRIOR APPLICATION NUMBER: US 09/847,208;
PRIOR FILING DATE: 2001-05-01;
NUMBER OF SEQ ID NOS: 13;
; SOFTWARE: PRESENCE for Windows Version 4.0;
; LENGTH: 569
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Best Local Similarity 100.
Matches 232; Conservative
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US-10-966-673-29
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US-10-617-619-7
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                                                                    PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSFGK 232
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                                                                                                                                   Sequence 1, Application US/09389782
Publication No. US20030144187A1
GENERAL INFORMATION:
APPLICANT: Wooden, Scott K.
APPLICANT: Mann, Michael B.
TITLE OF INVENTION: OGF Fusion Protein Compositions and Methods FILE REFERENCE: A-604
CURRENT APPLICATION NUMBER: US/09/389,782
CURRENT FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity 97.07
Matches 225; Conservative
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ORGANISM: Human
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LENGIH: 232
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US-10-617-619-7
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US-09-389-782-1
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APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Bill N
APPLICANT: Sun, Cecily R
TITLE OF INVENTION: Tec fusion proteins of human erythropoietin with high biological
TITLE OF INVENTION: activities
FILE REFERENCE: 025UN2001-A
CURRENT PLILING DATE: 2004-00-21
PRIOR PILING DATE: 2001-08-17
RIOR FILING DATE: 2001-08-17
RIOR FILING DATE: 2001-08-17
ROUMBER: OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.2
SEQ ID NO 26
LIBRORY: 232
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97.2%; Score 1225; DB 4; Length 232; 97.0%; Pred. No. 7.1e-90; ive 3; Mismatches 4; Indels
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GENERAL INFORMATION: APPLICANT: Kaye, Jonathan
                            97.08;
                                                      Matches 225; Conservative
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US-10-761-593A-26
       Query Match
Best Local Similarity
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APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Cecily R
TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-
TITLE OF INVENTION: increased biological activities
TITLE OF INVENTION: increased biological activities
FILE REFERENCE: 035UN2001
CURRENT APPLICATION NUMBER: US/10/800,497
CURRENT FILING DATE: 2004-03-15
PRIOR APPLICATION NUMBER: US/09/968,362
PRIOR PRILING DATE: 2001-10-01
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.1
SEQ ID NO 26
LENGTH: 232
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APPLICANT: Wilkinson, Beverley
TITLE OF INVENTION: SPEX COMPOSITIONS AND METHODS OF UFILE REFERENCE: TSRI 810.1
CURRENT PEPLICATION NUMBER: US/10/831,622
CURRENT FILING DATE: 2004-04-23
PRIOR APPLICATION NUMBER: US 60/467,206
PRIOR PILING DATE: 2003-04-30
SROFTWARE: PSECIED NOS: 113
SOFTWARE: PSECIED (OF Windows Version 4.0
SEQ ID NO 97
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97.0%; Pred. No. 7.1e-90;
iive 3; Mismatches 4;
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US-10-800-497-26
Sequence 26, Application US/10800497
Publication No. US20040259209A1
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Best Local Similarity 97.03
Matches 225; Conservative
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ORGANISM: Homo sapiens
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Sequence 26, Application US/10800449

Sequence 26, Application US/10800449

Publication No. US20040265973A1

Publication No. US20040265973A1

APPLICANT: Sun, Lee-Hwei K

APPLICANT: Sun, Cecily R

TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulaing factor L

TITLE OF INVENTION: Increased biological activities

FILE REPRENCE: 0350N2001

CURRENT FILING DATE: 2004-03-15

PRIOR APPLICATION NUMBER: US/10/906,449

CURRENT FILING DATE: 2001-10-01

PRIOR PILING DATE: 2001-10-01

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin version 3.1

SEQ ID NO 26
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; Sequence 97, Application US/10964215
; Publication No. US20050152893A1
; GENERAL INFORMATION:
    APPLICANT: Kaye, Jonathan
; TITLE OF INVENTION: METHODS AND MATERIALS FOR THE INHIBITION
; TITLE OF INVENTION: OF TRANSPLANT REJECTION
; TITLE OF INVENTION: OF TRANSPLANT REJECTION
; FILE REFERENCE: TSR 1810.2
; CURRENT APPLICATION NUMBER: US/10/964,215
; CURRENT FILING DATE: 2004-10-12
; PRIOR PILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/467,206
; PRIOR APPLICATION NUMBER: US 60/467,206
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains US-10-800-449-26
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Best Local Similarity 97.0%;
Matches 225; Conservative
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ORGANISM: Homo sapiens
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97.2%; Score 1225; DB 5; Length 232;
Best Local Similarity 97.0%; Pred. No. 7.1e-90;
Matches 225; Conservative 3; Mismatches 4; Indels
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7: /cgn2_6/ptodata/2/pubpaa/US11 NEW PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US11 NEW PUB.pep:*
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(c) 1993 - 2005 Compugen Ltd
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US-10-723-207-3

US-10-723-207-4

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ALIGNMENTS

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EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
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                                                                          APPLICANT: Lazar, Gregory Alan
TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
TITLE REPERENCE: 185831/US/2
CURRENT APPLICATION NUMBER: US/11/022,289
CURRENT FILLING DATE: 2004-12-21
PRIOR APPLICATION NUMBER: US 60/531,752
PRIOR APPLICATION NUMBER: US 60/531,752
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Parentin version 3.3
SEQ ID NO 11
LENGTH: 330
TYPE: PRT
US-11-022-289-11
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Pred. No. 1e-98;
3; Mismatches 4; Indels
; Sequence 11, Application US/11022289
; Publication No. US20050249723A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.2%;
97.0%;
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Best Local Similarity 97.0
Matches 225; Conservative
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APPLICANT: Heider, Karl-Heinz
TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
TITLE OF INVENTION: Cyclocaic CD44 Antibody Immunoconjugates and
TITLE OF INVENTION: Cyclocaic CD44 Antibody Immunoconjugates and
TITLE OF INVENTION: Cyclocaic CD44 Antibody Immunoconjugates and
TITLE OF INVENTION: Cyclocaic CA9000
FILE REFERENCE: 1/1383
CURRENT APPLICATION NUMBER: US/10/645,215
PRIOR FILING DATE: 2005-06-30
PRIOR APPLICATION NUMBER: EP 02 018 686.2
PRIOR PILING DATE: August 21, 2002
PRIOR PILING DATE: August 22, 2002
PRIOR PILING DATE: August 26, 2002
SOFTWARE: PAUGHTIN VOR. 2.1
SEQ ID NOS: 9
SOFTWARE: PAUGHTIN VOR. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/11016503
Pubblication No. US20050245447A1
GENERAL INFORMATION:
TULL OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
TITLE OF INVENTION: AND USING THEREOF
FILE REFERENCE: RG 710-A-US
CURRENT FILING DATE: 2004-12-17
PRIOR FILING DATE: 2001-12-06
PRIOR FILING DATE: 2001-12-06
PRIOR FILING DATE: 2001-12-06
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 1999-06-08
NUMBER OF SEQ ID NOS: 38
SOOTWARE: FASTSEQ FOR WINDOWS VERSION 3.0
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ORGANISM: Artificial Sequence
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Best Local Similarity 97.0
Matches 225; Conservative
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US-11-016-503-6
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                                                281 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
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US-10-949-720-190

Sequence 390, Application US/10949720

Publication No. US20050249736A1

GENERAL INFORMATION:
APPLICANT: Krasnoperov, Valery
APPLICANT: Reteaz, Nathalie
APPLICANT: Reteaz, Nathalie
APPLICANT: Reddy, Ramachandra
APPLICANT: Reddy, Ramachandra
APPLICANT: Reddy, Ramachandra

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APPLICANT: Reddy, Ramachandra

APPLICANT: Reddy, Ramachandra

APPLICANT: Rollow: DO:709-00-10

CURRENT APPLICATION NUMBER: US 60/454,432

PRIOR PILING DATE: 2003-03-12

PRIOR PILING DATE: 2003-03-12

PRIOR PILING DATE: 2003-03-12

PRIOR PILING DATE: 2004-03-12

NUMBER: OF SEQ ID NOS: 425

SOFTWARE: PSESC FOR Windows Version 4.0

LENGTH: 459

TWANDER CONTINENT APPLICANT: AND APPLICANT: AP
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Best Local Similarity 97.0%; Pred. No. 1.5e-98;
Matches 225; Conservative 3; Mismatches 4;
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; Sequence 8, Application US/11016503
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ORGANISM: Unknown
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NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMIGKEYKCKVSNKALPAPIEKT
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GENERAL INCRMATION:
GENERAL INCRMATION:
GENERAL INCRMATION:
TILLE OF INVENTION: WODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED
TITLE OF INVENTION: WODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED
TITLE OF INVENTION: WODIFIED CHIMERIC PROPERTIES AND METHODS OF MAKING
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF WAKING
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF WAKING
FILE REFERENCE: REG 710-A-US
CURRENT FILING DATE: 2004-12-17
PRIOR FILING DATE: 2001-12-06
PRIOR FILING DATE: 2001-12-06
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 1999-06-08
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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Publication No. US20050249723A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: 185831/US/2
CURRENT APPLICATION UNMBER: US/11/022,289
CURRENT FILING DATE: 2004-12-21
PRIOR PRILICATION NUMBER: US 60/531,752
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97.2%; Score 1225; DB 7;
Best Local Similarity 97.0%; Pred. No. 1.9e-98;
Matches 225; Conservative 3; Mismatches 4;
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SOFTWARE: Patentin version 3.3
SEQ ID NO 7
LENGTH: 551
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                                                                                                                                                                                                                                                                                                                                          LENGTH: 462
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US-11-022-289-7
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; Sequence 4, Application US/11016503
; Publication No. US20050245447A1
; GENERAL INFORMATION:
    APPLICANT: Nicholas J. Papadopoulos et al.
    TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED
    TITLE OF INVENTION: AND USING THEREOF
    TITLE OF INVENTION: WABER: US/11/016,503
    CURRENT FILING DATE: 2004-12-17
    PRIOR FILING DATE: 2001-12-06
    PRIOR FILING DATE: 2001-12-06
    PRIOR FILING DATE: 2000-05-23
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TITLE OF INVENTION: Fc POLYPEPTIDES WITH NOVEL Fc LIGAND BINDING SITES
FILE REFERENCE: 185831/US/2
CURRENT APPLICATION NUMBER: US/11/022,289
CURRENT FILING DATE: 2004-12-21
PRIOR FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.3
SEQ ID NO 8
LENGTH: 551
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97.0%; Pred. No. 1.9e-98;
iive 3; Mismatches 4;
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RESULT 10
US-11-022-289-5
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Publication No. US20050249723A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
FILE REPERENCE: 188931/US/2
CURRENT APPLICATION NUMBER: US/11/022,289
CURRENT FILING DATE: 2004-12-21
PRIOR FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.3
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                                                                                                                                                                                                               Length 557;
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PRIOR APPLICATION NUMBER: 60/138,133
PRIOR FILING DATE: 1999-06-08
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 557
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                                                                                                                                                 ORGANISM: Homo sapiens
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ORGANISM: Artificial
                                                                                                                                                       , ORGANISM: HC
US-11-016-503-4
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LENGTH: 557
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Sequence 5, Application US/11022289

Publication No. US20050249723A1

GENERAL INFORMATION:
TITLE OF INVENTION: CF POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
TITLE OF INVENTION: PC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
CURRENT APPLICATION NUMBER: US/11/022,289
CURRENT FILING DATE: 2004-12-21
PRIOR PRILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE PARENTIN Version 3.3
SEQ ID NO 5:
LENGTH: 557
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; Publication No. US20050249723A1
; GENERAL INFORMATION:
; TITLE LAZAT. LAZAT.
; TITLE OF INVENTION: Fc POLYPEPTIDES WITH NOVEL Fc LIGAND BINDING SITES
; FILE REFERENCE: 185831/US/2
; CURRENT APPLICATION NUMBER: US/11/022,289
; CURRENT FILING DATE: 2004-12-21
; PRIOR PPLING DATE: 2003-12-22
; PRIOR FILING DATE: 2003-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSFGK 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1225; DB 7;
Pred. No. 1.9e-98;
3; Mismatches 4;
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SOFTWARE: Patentin version 3.3
SEQ ID NO 6
LENGTH: 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 97.0%;
Matches 225; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
COTHER INFORMATION: Synthetic US-11-022-289-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
US-11-022-289-6
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US-10-949-720-389
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159 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPADIEKT 218
                                                               ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                              Sequence 2, Application US/11016503
| Sequence 2, Application US/11016503
| Publication No. US20050245447A1
| GENERAL INFORMATION:
| APPLICANT: Nicholas J. Papadopoulos et al.
| TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED
| TITLE OF INVENTION: MUD USING THEREOF
| TITLE OF INVENTION: AND USING THEREOF
| FILE REFERENCE: REG 710-A-US
| FRIOR APPLICATION NUMBER: US/10/009,852
| PRIOR FILING DATE: 2000-65-23
| PRIOR FILING DATE: 2000-65-23
| PRIOR FILING DATE: 1999-06-08
| NUMBER OF SEQ ID NOS: 38
| SOFTWARE: FastSEQ for Windows Version 3.0
| SEQ ID NO 2
| LENGTH: S67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   336 BPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISKTPEVTCVVVDVSHEDPEVKF
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Sequence 10, Application US/11016503
Publication No. US20050245447A1
GENERAL INFORMATION:
APPLICANT: Nicholas J. Papadopoulos et al.
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES WITH IMPROVED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
TITLE OF INVENTION: AND USING THEREOF
FILE REPERENCE: REG 710-A-05
CURRENT APPLICATION NUMBER: US/11/016,503
CURRENT FILING DATE: 2004-12-17
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Pred. No. 1.9e-98;
3; Mismatches 4;
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Best Local Similarity 97.0
Matches 225; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Zozulya, Sergey
APPLICANT: Zozulya, Sergey
APPLICANT: Redew, Nathalie
APPLICANT: Redew, Nathalie
APPLICANT: Redew, Ramachandra
APPLICANT: Redew, Ramachandra
APPLICANT: Gill, Parkash
TITLE OF INVENTION: POLYPEPTIDE COMPOUNDS FOR INHIBITI
TITLE OF INVENTION: ANGIOGENESIS AND TUMOR GROWTH
FILE REPERENCE: VASG-P02-002
CURRENT APPLICATION NUMBER: US/10/949,720
CURRENT FILING DATE: 2004-09-23
PRIOR FILING DATE: 2003-03-12
PRIOR FILING DATE: 2003-03-12
PRIOR PRILING DATE: 2003-03-12
PRIOR PRILING DATE: 2004-03-12
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97.0%; Pred. No. 2.8e-98;
cive 3; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
PRIOR APPLICATION NUMBER: US/10/009,852
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: PCT/US00/14142
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 1999-06-08
NUMBER OF SEQ ID NOS: 38
NUMBER OF SEQ ID NOS: 38
SEQ ID NO 10
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 389, Application US/10949720; Publication No. US20050249736A1; GENERAL INFORMATION:
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Matches 225; Conservative
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Best Local Similarity 97.0
Matches 225; Conservative
                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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ORGANISM: Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 SKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPP 181
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              600 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTYLHQDWLNGKEYKCKVSNKALPAPIEKT 659
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61 NWYUDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
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                                                                                                                                                                             Gaps
                                                                                                            181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                          720 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Predicted Mature Form of TLR9 EC260-Fc Fusion US-10-835-475-11
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96.8%; Score 1220; DB 1; Length 489;
Best Local Similarity 97.0%; Pred. No. 4.4e-98;
Matches 224; Conservative 3; Mismatches 4; Indels
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Search completed: November 30, 2005, 01:17:04 Job time : 5.62319 secs

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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                    Copyright
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- protein search, using sw model OM protein

; Search time 152.464 Seconds (without alignments) 922.194 Million cell updates/sec November 30, 2005, 00:34:13 Run on:

1707 1 FTPPTVKILQSSCDGGGHFP......HEAASPSQTVQRAVSVNPGK 320 US-09-847-208B-6 Perfect score: Sequence: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2443163 seqs, 439378781 residues Searched:

2443163 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB 8 Maximum DB 8

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sm

Genesed Database

geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2003s:* geneseqp2003s:* geneseqp2003s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	Aao19667 Human IgE	Human	Human	_	Fc (eps	Aar75225 Human IgE	Aar77241 Human IgE	Human		Add25768 Binding d	Human		Aap80291 Interleuk	Aao19666 Human IgE	Human	Aau80283 Human IgE	Aam50940 Human IgE	Aae35113 Human imm	Add48440 Human Pro	Ade97382 Human IgE	Aao19668 GE2 fusio	Human	Abg80562 Human IgE	Abp96592 Human IgE
SUMMAKIES	ID	AA019667	AAU80286	AAU80285	AAU80284	AAR83559	AAR75225	AAR77241	ADY21849	AAB03642	ADD25768	ADY21799	ADY21722	AAP80291	AA019666	AAM47863	AAU80283	AAM50940	AAE35113	ADD48440	ADE97382	AA019668	ABG94250	ABG80562	ABP96592
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d	Query Match		100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	1707	1707	1707	1707	1707	1707	1707	1707	1707	1707	1707	1707	1707	1707	1707	1707	1707	1707	1707	1707	1707	1707	1707	1707
	Result No.	7	7	м	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20			23	24

554 7 ADB597368 596 9 ADY22009 592 9 ADY21754 593 9 ADY21801 648 9 ADY21801 648 9 ADY21805 648 9 ADY21809 325 3 AAY79994 447 9 ADW24784 497 9 ADW24784 497 9 ADW24784 497 9 ADW24784 497 9 ADW24784 497 9 ADW268940 497 9 ADW268940 4983 1 AAR83582	Ade97368 Ady22009 Add221734 Ady21801 Ady21801 Ady21801 Ady21809 Ady21809 Ady21809 Ady21809 Ady21809 Ady21809 Ady21809 Ady21809 Ady21809 Ady21809 Ady208909 Ady208909 Ady208909 Ady208909 Ady208909 Ady208909 Ady208909 Ady208909 Ady208909 Ady208909 Ady208909
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ALIGNMENTS

Fcepsilon receptor; autoimmune disease; constant region; heavy chain; antiathmatic; antiallergic; antiinflammatory; dermatological; antiarthritic; antirheumatic; antidiabetic; neuroprotective; CH2-CH3-CH4 region. Human; IgE; immunoglobulin E; immunotherapy; immune disease; Human IgE heavy chain constant region CH2-CH3-CH4 portion. AAO19667 standard; protein; 320 AA (first entry) 28-MAR-2003 AA019667; RESULT 1 AAO19667

Homo sapiens.

WO200288317-A2.

07-NOV-2002.

01-MAY-2002; 2002WO-US013527.

01-MAY-2001; 2001US-00847208 24-OCT-2001; 2001US-00000439

(REGC) UNIV CALIFORNIA.

Zhu D; Zhang K, Saxon A,

WPI; 2003-103456/09.

New fusion molecules comprising polypeptide sequences that bind to IgG inhibitory receptor and native IgE receptor, useful for treating IgE-mediated hypersensitivity reactions, e.g. asthma or allergies, or autoimmune diseases.

Claim 21; Fig 6; 116pp; English.

The present invention relates to a fusion molecule comprising a first polypeptide sequence capable of specific binding to a native IgG inhibitory receptor consisting of an immune receptor tyrosine-based inhibitory motif (ITM), expressed on mast cells, basophils or B cells, functionally connected to a second polypeptide sequence capable of specific binding directly or indirectly to a native IgE receptor (FcepsilonR). Also provided are nucleotide sequences encoding such a

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RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
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fusion protein. The fusion molecules and compositions are useful for treating an IgE-mediated biological response, preferably an IgE-mediated hypersensitivity reaction, such as asthma, allergic rhinitis, atopic dermatitis, severe food allergies, chronic urticaria, angioedema or anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis, type-I diabetes mellitus, or multiple sclerosis, and for preventing of, or symptoms resulting from, a type I hypersensitivity reaction in a subject recedving immunotherapy. The present sequence is the human IgE heavy chain constant region CH2-CH3-CH4 portion
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100.0%; Pred. No. 4.1e-129;
ive 0: Mismatches 0; Indels
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This invention relates to a novel method for inducing an immune response against autologous immunoglobulin E (IgE) in an animal. The method comprises effecting simultaneous presentation of cytotoxic T lymphocyte (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell epitope (TH epitope) which is foreign to the animal, by antigen cell presenting cells (APCs) of the animal's immune system. The epitopes of the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autologous IgE in a naimal, which is useful for dwarregulating autologous IgE in the animal, which is useful in the prevention and treatment of allergic diseases such as anaphylaxis, allergic rhinitis, asthma and aropic dermatitis. The present sequence represents the human IgE heavy chain C2-C3-C4 domains optimised for expression in an B. Coli system, this sequence was used to create the epitopes of the invention
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                                 Inducing immune response against autologous immunoglobulin E in an animal, by effecting simultaneous presentation of cytotoxic I lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin.
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100.0%; Pred. No. 4.2e-129;
ive 0; Mismatches 0;
                                                                                                                  Disclosure; Page 112-113; 151pp; English.
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Best Local Similarity
Matches 320; Conserv
N-PSDB; ABK51134.
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IgE; allergy; human; antiallergic; immunosuppressive; antianaphylactic; antiathmatic; dermatological; antiinflammatory; immunoglobulin E; IgE; vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis; heavy chain C domain.
                               Human IgE heavy chain C2-C3-C4 domains.
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15-SEP-2000; 2000US-0232831P.
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 This invention relates to a novel method for inducing an immune response against autologous immunoglobulin E (IgE) in an animal. The method comprises effecting simultaneous presentation of cytotoxic T lymphocyte (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell epitope and/or B-cell epitope derived from IgE, and T helper cell epitope (TH epitope) which is foreign to the animal, by antigen presenting cells (APCs) of the animal's immune system. The epitopes of the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autologous IgE in the animal, which is useful for downregulating autologous IgE in the animal. This method is useful in the prevention and treatment of allergic diseases such as anaphylaxis, allergic rhinitis, autologous IgE in the animal. The present sequence represents the human igE heavy chain C2-C3-C4 domains optimised for expression in a mammalian system, this sequence was used to create the epitopes of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1707; DB 5;
100.0%; Pred. No. 4.2e-129;
iive 0; Mismatches 0;
                                                                                                                                                                        Gautam A;
                                                                                                                                                                                                                                                                                                                           Disclosure; Page 108-110; 151pp; English
                                                                                                                                                                      Voldborg B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HEAASPSQTVQRAVSVNPGK 320
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                                                      06-SEP-2001; 2001WO-DK000579.
                                                                                     2000DK-00001326.
2000US-0232831P.
                                                                                                                                                                        Klysner S, Von Hoegen P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 320; Conservative
                                                                                                                                                                                                         WPI; 2002-383033/41.
                                                                                                                                        (PHAR-) PHARMEXA AS
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                                                                                                                                                                                                                         N-PSDB; ABK51133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 323 AA;
                                                                                                     15-SEP-2000;
                                                                                       06-SEP-2000;
                      14-MAR-2002
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212. .215 /note= "Linker between domains C3 and C4" 216. .317

/note= "IgE heavy chain C4 domain"

Gautam A;

Voldborg B,

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/note= "Epitope including C3C4 linker"

/note= "Epitope in FG loop" 210. 218 'note= "Epitope in DE loop"

.206

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C2 and

112. .211 /label= IgE heavy chain C3 domain 139. .145

'note= "Linker between

/note= "Epitope in BC loop" 167. 175

note= "Epitope including C2C3 linker"

'note= "IgE heavy chain C2 domain"

.114 .111

Location/Qualifiers

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This invention relates to a novel method for inducing an immune response against autologous immunoglobulin E (IgE) in an animal. The method comprises effecting simultaneous presentation of cytocoxic T lymphocyte (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell epitope (TH epitope) which is foreign to the animal, by antigen presenting cells (APCs) of the animal's immune system. The epitopes of the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autologous IgE in an animal, which is useful for downregulating autologous IgE in the animal. This method is useful in the prevention and treatment of allergic diseases such as anaphylaxis, allergic rhintis, aschma and atopic dermatitis. The present sequence represents the human IgE heavy chain C2-C3-C4 domains used to create the epitopes of the
                                                                        Inducing immune response against autologous immunoglobulin E in an animal, by effecting simultaneous presentation of cytotoxic \tau lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1707; DB 5; Length 323;
Pred. No. 4.2e-129;
                                                                                                                                                                                                                                                                        Disclosure; Page 105-106; 151pp; English
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WPI; 2002-383033/41.
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Best Local Similarity
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AAU80284 standard; protein; 323

AAU80284

AAU80284;

glycosylation

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Gaps

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glycosylated Fc(epsilon) fragment. Altering the pattern of glycosylation unmasks new antigenic sites thus rendering the Fc fragment immunogenic and able to induce antibodies that recognise native IgB but do not form histamine-releasing complexes. The Fc fragments can be used in antiallergenic vaccines to modulate the intensity of immune responses
                                                                                                                                                                                                                                                                                                                                         FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
                                                                                                                                                                                                                                                                                                                  GELASTOSELTLSOKHWLSDRTYTCOVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD
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                                                                                                                                                                                                                                           FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
                                                                                                                                                                Length 324;
                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           224-547) mutant sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or deletion'
                                                                                                                                                                  Query Match 100.0%; Score 1707; DB 2; Best Local Similarity 100.0%; Pred. No. 4.2e-129; Matches 320; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "glycosylation site" Misc-difference 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "any AA or deletion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Val224
/note= "any AA or deletion"
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/note= "Ala, any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR75225 standard; protein; 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human IgE Fc chain (amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "any AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Asp228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IgE Fc fragment; antiallergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
(first entry)
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                                                                                                                                  Sequence 324 AA;
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                                                                                             mediated by IgE
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10-NOV-1995
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                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fc(epsilon); antibody; human; myeloma; probe; IgE; tryptophan promoter; constant heavy region; E.coli; glycosylation; antigenic; immunogenic; histamine; anti-allergenic; vaccine; immune response.
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for
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                                                                                                               GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD
                                                                                                                                                                                                                      LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
                                                                                                                                                                                                                                                              RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
                                                                          PTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
                                                                                                                                                                                     LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
                                          FTPPTVKILQSSCDGGGHFPPT1QLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antiallergic vaccine contg. polypeptide fragment of IgE heavy chain epitope(s) not present in native IgE, also derived antibodies for treating or preventing allergies, inflammatory immune disease, etc.
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     0; Indels
     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                & VACCINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fc(epsilon) CH2'-CH4 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR83559 standard; protein; 324 AA
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     Conservative
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N-PSDB; AAT01865.
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   320;
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                                                                                                                                                                                        The sequence represents a mutant sequence of a human IgE-Fc chain (amino acids 224-547) which is of sufficient length to bind Fc-epsilon RI and/or Fc-epsilon FII IgE receptor sites on human cells. The protein is useful in the study and treatment of allergy. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                     RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                   NEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV 300
                                                                                                                                                  - useful
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                                                                                                                                                                                                                                                                                                                                                     LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
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                                                                                                                                                glycosylated polypeptide(s) contg. parts of human IgE-Fc
                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                        Length 325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human IgE Fc chain (amino acids 224-547) wild-type sequence.
                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                       100.0%; Score 1707; DB 2;
100.0%; Pred. No. 4.2e-129;
iive 0; Mismatches 0;
        /note= "glycosylation site"
                                                                                                            Owens RJ;
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                                                                                                                                                                          Disclosure; Page 6; 55pp; English.
                                                                                                            Young RJ, Sutton BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR77241 standard; protein; 325
/label= Asn394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IgE Fc fragment; antiallergic
                                                                                    (THRE-) 31 RES EXPL LTD.
(CLLT ) CELLTECH THERAPEUTICS
                                                      94WO-GB002561
                                                                     93GB-00024013
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                                                                                                                                                          and treat allergy
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                                                                                                                            WPI; 1995-206936/27
                                                                                                                                                                                                                                                              al Similarity
320; Conserv
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                        WO9514779-A1
                                                      22-NOV-1994;
                                                                     22-NOV-1993;
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61 GELASTOSELTLSOKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence represents the wild-type sequence of a human IgE-Fc chain (amino acids 224-547) which is of sufficient length to bind Fc-epsilon RI and/or Fc-epsilon FII IgE receptor sites on human cells. The sequence is preferably mutated (see AAR75225) to represent a protein encoding a protein where Cys225 is mutated, optionally together with Val224, Ser226 and Arg227. The protein is useful in the study and treatment of allergy. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
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                                                                                                                                                          /note= "glycosylation site"
                                                                             gite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Owens RJ;
                                                                          /note= "glycosylation
172
/label= Asn394
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Location/Qualifiers
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(CLLT ) CELLTECH THERAPEUTICS
                                                    /label= Asn371
                                                                                                                                                                                                                                                                                                                     94WO-GB002561,
                                                                                                                                                                                                                                                                                                                                                                      93GB-00024013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1995-206936/27
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                        Misc-difference
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ADY21849 standard; protein; 327 AA. Human IgE CH2-CH3-CH4 region. (first entry) 05-MAY-2005

thrombocytopenic purpura; hemostatic; hematological disease; multiple sclerosis; neuroprotective; neurological disease; myasthenia gravis; muscular-gen.; bacterial infection; fungal infection; fungicide; viral infection; virucide; parasitic infection; antiparasitic; Antibacterial; Virucide; Antiparasitic; Fungicide; Immunotherapy; antibody engineering; cancer; neoplasm; cytostatic; immune disorder; graves disease; antihyroid; endocrine disease; hashimotos disease; immunosuppressive; rheumatoid arthritis; antiarthritic; antirheumatic; inflammation; musculoskeletal disease; systemic lupus erythematosus; antiinflammatory; dermatological; dermatological disease; metabolic disorder; sjoegrens syndrome; coular disease; fusion protein.

Homo sapiens

WO2005017148-A1

24-FEB-2005

24-DEC-2003; 2003WO-US041600.

26-JUL-2003; 2003US-00627556.

(TRUB-) TRUBION PHARM INC

Thompson PA; Ledbetter JA, Hayden-Ledbetter MS,

WPI; 2005-182370/19. N-PSDB; ADY21848,

New non-naturally occurring single chain protein comprising polypeptides with binding domain, connecting regions and N-terminally truncated immunoglobulin, having immunological activity, useful for neutralizing infectious agent.

Disclosure; Page 365; 590pp; English.

The invention relates to a non-naturally occurring ships contain protecting capable of binding to a target molecule, the binding domain polypeptide capable of binding to a target molecule, the binding domain polypeptide capable of binding to a target molecule, the binding domain polypeptide comprising a heavy chain variable region, which comprises an anahon acid substitution or deletion at one or more amino acid residues, a second polypeptide comprising a connecting region attached to the first complete or an a thind polypeptide comprising an N-terminally truncated immunoglobulin heavy chain constant region polypeptide attached to the second polypeptide, where the non-naturally occurring single-chain contains a target cell population in a subject (involving administering content a target cell population in a subject (involving administering to the subject a procein that is less than 150 kb, which involves treating the target cell population with a first protein or peptide that capable of at least coll population with a second protein or peptide molecule is directly connected to the second protein or peptide molecule is directly connected to the second protein or peptide molecule or, optionally, the first protein or peptide molecule and the second protein or peptide molecule and where the protein or peptide molecule and the second protein or peptide molecule and where the protein molecule is not an antibody, a member of the TNF family, and is not a radioisotope), depleting cells in an animal containing the polymolecule, a recombinant vector capable of expressing the polypoptide, expressing the polypeptide, capable of capable of expressing the polypoptide, in composition with one or more invention relates to a non-naturally occurring single chain protein

additional therapeutic compounds, displaying recombinant molecules (which molecules include a native or engineered immunoglobulin heavy chain crafion, the improvement comprising an immunoglobulin heavy chain region that includes one or more mutation, substitution, alteration, and/or deletion at one or more amino acid residue corresponding to positions 9, 10,11,12, 108, 110, and 112 in the heavy chain variable region) and a non-naturally occurring single chain antigen-binding protein having a mutation chosen from a list given in the specification. The polypeptides of the invention comprise single communoglobulin hinge region (wild-type or mutants where the cysteines are immunoglobulin (19d, 19E or 10g) heavy chain constant region (CH) which may also have mutations in CH2 (e.g. T256N) or a truncated CH3 (e.g. T4 cm), a 4 amino acid deletion). The polypeptide may be further linked to a non-antibody protein such as the transmembrane and cytoplasmic tail (TN/CT) of caspase-3, caspase-8 or CD80. The fusion polypeptides are useful for neutralization of an infectious agent (where the infectious agent is a bacterium, a virus, a parasite, or a fungus) and also for treatment of cancer, immune disorders, Grave's disease, Hashimoto's such are the contradict of arthritis, systemic lupus erythematosus. Slocery, when the contradict of the contradict of an infectious agent (where the infectious cyparance) thrombocytopenic purpura, multiple sclerosis and myasthenia cyparance. The present sequence is an antibody perion protein of the invention of the invention of the invention of the invention of the manner of contradicts and myasthenia contradicts and myasth ö 61 GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD 120 127 180 187 240 247 300 248 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV 307 9 63 68 GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD 188 RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 1 FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE 8 FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTOE 121 LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKBEKQRNGTLTVTSTLPVGT 181 RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 241 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV ninge, CH region, VL or VH) used in a fusion protein of the invention Gaps ö Length 327; Indels 100.0%; Score 1707; DB 9; 100.0%; Pred. No. 4.3e-129; iive 0; Mismatches 0; AAB03642 standard; protein; 331 AA HEAASPSQTVQRAVSVNPGK 320 308 HEAASPSQTVQRAVSVNPGK 327 Query Match 100. Best Local Similarity 100. Matches 320; Conservative Sequence 327 AA; 301 RESULT 9 AAB03642 8888888888888888888888888888 셤 원 g 셤 ò 셤 ò ò ò ò

Human, immunoglobulin E, 1gE, vaccination, infection, allergy, asthma, eczema, immunogenic peptide. Human IgE heavy chain constant regions 2, 3 and 4. (first entry) 22-NOV-2000 Homo X B X S X & X E X B X B X S X B

AAB03642;

WO200025722-A2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191
                                                                                                                                                                                       The present sequence is an immunogenic peptide consisting of the heavy chain constant regions 2, 3 and 4 of the human IgE. It was used to construct a number of immunogenic peptides which consisted of regions of IgE from different mammals, which appear to cause a stronger polyclonal anti-self IgE response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of different heavy chain constant regions, can be used for vaccination in humans, against bacterial and viral infections and allergies, such as
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                                                                                                                                  Immunogenic polypeptides useful for preventing the harmful effects of immunoglobulin \boldsymbol{E} in mammals.
                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                   100.0%; Score 1707; DB 3; Length 331; 100.0%; Pred. No. 4.3e-129; ive 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                             asthma, fur, pollen and food allergies and eczema
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                                                                                                                                                                     Disclosure; Fig 1; 50pp; English.
                                        98US-0106652P.
                                                                        (RESI-) RESISTENTIA PHARM AB
                     99WO-SE001896
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                                                                                                                                                                                                                                                                                                                                          Matches 320; Conservative
                                                                                                                   WPI; 2000-365342/31.
                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                 Sequence 331 AA;
                      21-OCT-1999;
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was maintedy dependent call indicated cytoconicity, NACC complement fixation; mailtanar condition; B-cell disorder; maintenance carcinome, sarcome, maintenated arthritis; myacthenia gravis; Grave's disease; type I diabetes mellitus; myacthenia gravis; type I diabetes diabetes; type I diabetes diabe

Sequence 331 AA;

100.0%; Score 1707; DB 7; Length 331;

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                                                               GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD 120
                                                                           GELASTOSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD 127
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                                                                                                             LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
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                          1 PTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
          Gaps
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         0; Indels
Pred. No. 4.3e-129;
         Mismatches
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multiple sclerosis, neuroprotective, neurological disease, myasthenia gravis, muscular-gen.; bacterial infection, fungal infection, fungicide, viral infection, virucide, parasitic infection, antiparasitic, antibody engineering; cancer; neoplasm; cytostatic; immune disorder; graves disease; antithyroid; endocrine disease; hashimotos disease; immunosuppressive; rheumatoid arthritis; antiarthritic; antirheumatic; inflammation; musculoskeletal disease; systemic lupus erythematosus; antiinflammatory; dermatological; dermatological disease; metabolic disorder; sjoegrens syndrome; ocular disease; thrombocytopenic purpura; hemostatic; hematological disease; Antibacterial; Virucide; Antiparasitic; Fungicide; Immunotherapy; fusion protein

Homo sapiens

WO2005017148-A1.

24-FEB-2005.

24-DEC-2003; 2003WO-US041600.

26-JUL-2003; 2003US-00627556

(TRUB-) TRUBION PHARM INC.

Thompson Ledbetter JA, Hayden-Ledbetter MS,

WPI; 2005-182370/19.

N-PSDB; ADY21798

PA;

New non-naturally occurring single chain protein comprising polypeptides with binding domain, connecting regions and N-terminally truncated immunoglobulin, having immunological activity, useful for neutralizing infectious agent.

Disclosure; Page 352; 590pp; English.

The invention relates to a non-naturally occurring single chain protein (I) comprising a first polypeptide having a binding domain polypeptide capable of binding to a first polypeptide having a binding domain polypeptide capable of binding to a target molecule, the binding domain polypeptide capable of binding to a target molecule, the binding domain polypeptide comprising a heavy chain variable region, which comprises an amino acid mubsitution or delation at one or more amino acid residues, a second to polypeptide comprising a conservation of the first polypeptide comprising a conservation of the first polypeptide attached to the second polypeptide where the non-naturally occurring single-chain protein is capable of an immunological activity, Alsa included are reducing a target cell population with a first protein or peptide that confidence a protein that is less than 150 kD, which involves to the subject a protein that is less than 150 kD, which involves to the subject a protein or peptide molecule and treating the target cell population with a second protein or peptide molecule are linked by a third protein or peptide molecule are linked by a third protein or peptide molecule and where the connected to the second protein or peptide molecule are linked by a third protein or peptide molecule are linked by a third protein or peptide molecule are linked by a third protein or peptide molecule are linked by a third protein or peptide molecule are linked by a conjugated with a bacterial toxin, a cylotoxic drug, or a radiologroppy depletion or peptide molecule and where the conjugated with a bacterial toxin, and whore the protein or peptide molecule and is not conjugated with a bacterial toxin, and where the companishing the polymetical with a bacterial toxin, and or the polymetical and and an animally. A polymetical propertied a native or engineering an immunollobulin heavy companishing the polymetical are region, the improvement comprising an immunollobulin indeed a native or more amino acid residue comprise singl disease, rheumatoid arthritis, systemic lupus erythematosus, Sjoegren' syndrome, thrombocytopenic purpura, multiple sclerosis and myasthenia gravis. The present sequence is an antibody peptide or fragment (scFV, VL or VH) used in a fusion protein of the invention treatment of cancer, immune disorders, Grave's disease, Hashimoto's ninge, CH region,

Sequence 331 AA;

Gaps ; 0 Length '331; Indels ; Score 1707; DB 9; ; Pred. No. 4.3e-129; 0; Mismatches 0; 100.0%; Best Local Similarity Lov. Matches 320; Conservative Similarity Query Match Best Local S

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FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE

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(1) comprising a first polypeptide having a binding domain polypeptide capable of binding to a target molecule, the binding domain polypeptide comprising a heavy chain variable region, which comprises an amino acid substitution or deletion at one or more amino acid residues, a second polypeptide comprising a connecting region attached to the first polypeptide, and a third polypeptide comprising an N-terminally truncated immunoglobulin heavy chain constant region polypeptide attached to the second polypeptide, where the non-naturally occurring single-chain protein is capable of an immunological activity. Also included are reducing a target cell population in a subject (involving administering to the subject a protein that is less than 150 kD, which involves treating the target cell population with a first protein or peptide that
RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
                         RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 247
                                                                            NFMPEDISVQW1.HNEVQL.PDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV 300
                                                                                                  248 NFWPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           myasthenia gravis, muscular-gen.; bacterial infection; fungal infection; fungicide; viral infection; virucide; parasitic infection; antiparasitic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New non-naturally occurring single chain protein comprising polypeptides with binding domain, connecting regions and N-terminally truncated immunoglobulin, having immunological activity, useful for neutralizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a non-naturally occurring single chain protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibacterial; Virucide; Antiparasitic; Fungicide; Immunotherapy; antibody engineering; cancer; neoplasm; cytostatic; immune disorder; graves disease; antihyroid; endocrine disease; hashimotos disease; immunosuppressive; rheumatoid arthritis; antiarthritic; antirheumatic; inflammation; musculoskeletal disease; systemic lupus erythematosus; antiinflammatory; dermatological disease; thrombocytopenic purpura; hemostatic; hematological disease; thrombocytopenic purpura; hemostatic; hematological disease; multiple sclerosis; neuroprotective; neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thompson PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 321; 590pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Human IgE Fc (CH2-CH3-CH4) protein.
                                                                                                                                                                                                                                                                                                          ADY21722 standard; protein; 331 AA
                                                                                                                                                               HEAASPSQTVQRAVSVNPGK 320
                                                                                                                                                                                   24-DEC-2003; 2003WO-US041600.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TRUB-) TRUBION PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fusion protein.
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ö 241 NPMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV 300 GELASTOSELTLSOKHWLSDRTYTCOVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD 120 68 GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD 127 LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT 180 187 RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240 9 67 hinge, CH region, VL or VH) used in a fusion protein of the invention Gaps ö 100.0%; Score 1707; DB 9; Length 331; 100.0%; Pred. No. 4.3e-129; Live 0; Mismatches 0; Indels 0; 301 HEAASPSQTVQRAVSVNPGK 320 308 HEAASPSQTVQRAVSVNPGK 327 Query Match Best Local Similarity 100. Matches 320; Conservative Sequence 331 AA; -188 248 121 181 ઠે 셤 g ઠે 셤 ò g ઠે 셤 ò g ð

RESULT 13 AAP80291

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Sequence 427 AA;
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                                                                                                                                                                                                                                                                                                                                                                                         Saxon A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Fused protein for allergy treatment - comprising interleukin-2 N-terminal residues, a linker and human immunoglobulin \rm E \rm Fc fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This fusion protein has a low toxicity and is useful in therapy for allergy induced by 19E. It can be used in the treatment of allergic dermatosis, atopic dermatitis or bronchial asthma. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
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                                                                                                     interleukin-2; IgE Fc receptor; fusion protein; asthma; dermatitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1707; DB 1; Length 367; 100.0%; Pred. No. 4.9e-129; ive 0; Mismatches 0; Indels 0.
                                                                                                                                                               l. .20
/label= IL-2 leader seguence
                                                                                                                                                                           Interleukin-2/IgE Fc fusion protein.
                                                                                                                                                 Location/Qualifiers
AAP80291 standard; protein; 367 AA.
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                                                                                                                                                                                                           32. .36
/label= linker
37. .367
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87JP-00232295.
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                                                         (first entry)
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Matches 320; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       Nishimura O;
                                              (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 367 AA;
                                                                                                                                                                                                                                                                                                        27-NOV-1987;
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18-SEP-1987;
                                            25-MAR-2003
06-DEC-1990
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                                                                                                                            Synthetic
                    AAP80291;
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                                                                                                                                                            Peptide
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The present invention relates to a fusion molecule comprising a first polypeptide sequence capable of specific binding to a native IgG inhibitory receptor consisting of an immune receptor tyrosine-based inhibitory motif (ITIM), expressed on mast cells, basophils or B cells, functionally connected to a second polypeptide sequence capable of specific binding directly or indirectly to a native IgE receptor (FeepsilonR). Also provided are nucleotide sequences encoding such a fusion protein. The fusion molecules and compositions are useful for treating an IgE mediated biological response, preferably an IgE-mediated chological response, preferably an IgE-mediated choraction, such as methna, allergic rhinitis, atopic dermattis, severe food allergies, chronic urticaria, angioedema or anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis, crype-I diabetes mellitus, or multiple sclerosis, and for preventing of, or symptoms resulting from, a type I hypersensitivity reaction in a construction of the const
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTFGTINITWLEDGQVMDVDLSTASTTQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; IgE; immunoglobulin E; immunotherapy; immune disease; Forepsilon receptor; autoimmune disease; constent region; heavy chain; antiathmatic; antiallergic; antiinflammatory; dermatological; antiathritic; antirheumatic; antidiabetic; neuroprotective.
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100.0%; Pred. No. 6e-129;
ive 0; Mismatches 0;
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                                                                 348 HEAASPSQTVQRAVSVNPGK 367
301 HEAASPSQTVQRAVSVNPGK 320
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24-OCT-2001; 2001US-00000439.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an immunoadhesin comprising: (a) a chimeric intercellular adhesion molecule (ICAM)-1 comprising a rhinovirus receptor protein linked to at least a portion of an immunoglobulin heavy chain, and (b) optionally a J chain and secretory component associated with the chimeric ICAM-1 molecule. The immunoadhesin has plant-specific chimeric ICAM-1 molecule activity. The immunoadhesin is useful for reducing infection by human rhinovirus (HRV) and hence the initiation or spread of the common cold by HRV. The immunoadhesin binds to HRV and release of the common cold by HRV. The immunoadhesin binds to HRV and release of viral RNA and formation of empty capsids. Expression of the immunoadhesin in plants would be tetrameric, rather than dimeric. Immunoadhesin having multiple binding sites have a higher effective affinity for the virus, thereby increasing the effectiveness of the immunoadhesin. Association of secretory component and immunoglobulin J chain increases the stability of the immunoadhesin in the mucosal continuous chain increases the stability of the immunoadhesin in the mucosal continuous chain increases the stability of the immunoadhesin in the mucosal continuous chain increases the stability of the immunoadhesin in plants than in
                                                                                                                                                          NEMPEDISVOMLANEVOLPDARHSTTOPRKTKGSGFFVFSRLEVTRAEWEGKDEFICRAV 300
                               LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT 180
                                                                                                              Immunoadhesin for treating human rhinovirus infection comprises chimeric intercellular adhesion molecule-1, and optionally a J chain and secretory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; immunoadhesin; intercellular adhesion molecule; ICAM-1;
human rhinovirus; immunoglobulin heavy chain; J chain; HRV; common cold;
 GELASTQSELTLSQXHWLSDRTYTCQVTYQGHTFEDSTXKCADSNPRGVSAYLSRPSPFD
                                                  RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Ig-E heavy chain constant region amino acid sequence.
                                                                                                                                                                                                                                                                                                                                          AAM47863 standard; protein; 428 AA
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                                                                                                                                                                                                                                            (PLAN-) PLANET BIOTECHNOLOGY INC
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N-PSDB; ABA05278.
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                                                                                                                                                                                                                                                       GELASTOSELTLSOKHWLSDRTYTCOVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD
                                                                                                                                                                                                                                                                                                                                              181 RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
                                                                                                                                                                                      1 FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
                                                                                                                                                                                                                                                                                                                           LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
animal cell culture and production in plants is safer for human use, since plants are not known to harbor any animal viruses. The present sequence is that of a human immunoglobulin protein sequence, useful
                                                                                                                                                    ö
                                                                                                                   7; DB 5; Length 428;
6e-129;
les 0; Indels 0;
                                                                                                                   100.0%; Score 1707;
100.0%; Pred. No. 6e-
ive 0; Mismatches
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Job time : 154.464 secs
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                                                                                                                                          Best Local Similarity 100.
Matches 320; Conservative
                                                                                                                                        Similarity
                                                                                     Sequence 428 AA;
                                                      the invention
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Best Local
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5.1.6
Compugen Ltd.
GenCore version (c) 1993 - 2005
             Copyright
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sw model using protein search, OM protein ; Search time 30.1449 Seconds (without alignments)
1021.378 Million cell updates/sec November 30, 2005, 00:46:45 Run on:

Title: Perfect score:

US-09-847-208B-6 1707 1 FTPPTVKILQSSCDGGGHFP......HEAASPSQTVQRAVSVNPGK 320 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		epsilon-		epsilon	epsilon		epsilon	epsilon	epsilon	Y heavy		gamma		mu che		gamma 1 o	mu chain	mu chain	gamma 3	gamma-2 (Ig gamma 2a chain	oclonal a	mu chain	Ig mu chain C regi	gamma	þe	mu heavy ch	mu chain C	Ig mu chain - shee
	ΩI	Енни	I36948	EHRT	EHMS	S38864	EHMSS	PH1215	PH1216	E53116	B46529	S31436	800390	S04845	MHMS	A24976	147158	MHMSM	MHHY	147161	G2HU	147159	PC4436	S03961	837768	147160	S22080	MHHUBT	S25644	825705
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	Length	428	426	429	388	548	423	227	243	115	572	433	504	549	455	455	328	476	454	328	326	328	444	457	453	328	470	391	343	592
ф	Query Match	100.0	96.3	46.5	44.0	41.9	39.7	33.7	33.7	33.4	27.6	27.5	27.5	26.7	25.7	25.7	25.4	25.2	25.1	25.1	24.4	24.3	24.3	24.2	24.2	24.1	24.1	24.0	24.0	24.0
	Score	1707	1644.5	793	751	716	678.5	576	576	570	471	470	469	455.5	439.5	439.5	433	430.5	428.5	428	416	415	414	413.5	413	412	411.5	410	409.5	409
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Ig mu chain C regi	Ig gamma-2 chain C	Ig heavy chain - h	Ig mu chain C regi	Ig gamma-1 chain C	Ig gamma 4 chain c	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-1 chain C	Ig gamma-1 chain C	Ig mu chain C regi	Ig mu chain precur	Ig gamma-2b chain	Ig gamma-1 chain -	Ig gamma-2a chain
MHRB	G2GP	S15590	MHHU	G1MS	147162	G2MSA	S37483	840295	СННО	G1MSM	MHRBM	S14683	S01321	S31459	G2MSAM
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458	329	474	452	324	277	330	469	446	330	393	479	627	475	472	399
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405.5	404.5	404	402.5	402	400.5	399	399	398	397.5	397	396.5	396.5	396	395.5	394
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ALIGNMENTS

Ig epsilon chain C region - human

Cypecies: Homo sapies (man)
Cypecies: Homo sapies (man)
Cypecies: Homo sapies (man)
Cypecies: Homo sapies (man)
Cypecies: Har-1981 #sequence revision 13-Jun-1983 #text change 09-Jul-2004
Cypacesion: A22771; A23195; FH1214; A93491; A90824; A94418; B93933; S02438; A53116; C46
R;Flanagan, J.G.; Rabbitts, T.H.
EMBO J. 1, 655-660, 1982
A;Title: The sequence of a human immunoglobulin epsilon heavy chain constant region genê
A;Reference number: A22771; MUID:84236029; PMID:6234164
A;Residues: 1-428 cFLLA
A;Residues: 1-428 cFLLA
A;Residues: 1-428 cFLLA
A;Cross-references: UNIPROT:P01854; UNIPARC:UPI000004BB48; GB:L00022; GB:J00227; GB:V005
R;Ueda, S.; Nakai, S.; Nishida, Y.; Hisajima, H.; Honjo, T.
EMBO J. 1, 1539-1544, 1982
A;Title: Long terminal repeat-like elements flank a human immunoglobulin epsilon pseudoglascence number: A23195; MUID:84207910; PMID:632776

A; Molecule type: DNA A; Residues: 2-428 < UED>

A;Cross-references: UNIPARC:UP10000173783; GB:J00222; NID:g184755
R;Zhang, K.; Saxon, A.; Max, B.B.
J; Exp. Med. 176, 233-243, 1992
A; Exp. Med. 176, 233-243, 1992
A; Exp. Two unusual forms of human immunoglobulin B encoded by alternative RNA splicing A;Reference number: PH1214; MUID:92308839; PMID:1613458
A;Accession: PH1214

A; Molecule type: DNA
A; Residues: 320-428 <ZHA>
A; Residues: 320-428 <ZHA>
A; Cross-references: UNIPARC:UPI000014452D; EMBL:X63693; GB:S38668; NID:g32987
A; Cross-references: UNIPARC:UPI00001452D; EMBL:X63693; GB:S38668; NID:g32987
B; Seno, M.; Kurokawa, T.; Onda, H.; Sasada, R.; Igarashi, K.; Kikuchi, M.; Sudincleic Acids Res. 11, 719-726, 1983
A; Title: Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon ch# A; Reference number: A93491; MUID:83168897; PMID:6300763
A; Accession: A93491
A; Residues: 1-428 <SEN>

A,Cross-references: UNIPARC:UP1000004BB48; GB:L00022; GB:J00227; GB:V00555; NID:g185035 R;Max, E.E.; Battey, J.; Ney, R.; Kirsch, I.R.; Leder, P. Gell 29, 691-699, 1992 A; Title: Duplication and deletion in the human immunoglobulin epsilon genes. A,Reference number: A90824; MUID:83001945; PMID:6288268

A;Accession: A90824

A;Molecule type: DNA A;Residues: 1.358, TL',360-428 <MAX> A;Residues: 1.358, TL',360-428 <MAX> A;Coos-references: UNIPARC:UP10000173784; GB:J00222; NID:g184755 A;Croos-reference difference may be due to polymorphism A;Note: this sequence difference may be due to polymorphism R;Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H. i. Johansson, S.G.O.; Von Bahr-Lindstrom, H. in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.1-\$

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301 HEAASPSQTVQRAVSVNPGK 320
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Best Local Similarity 97.2%;
Matches 311; Conservative
                                                              Query Match 100.
Best Local Similarity 100.
Matches 320; Conservative
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A; Residues: 401-428 cHE3>
A; Residues: 401-428 cHE3>
A; Cross-references: UNIPARC:UPI000113EF5; GB:S53497; NID:g263162; PIDN:AAB24855.1; PID: A; Experimental source: B cell myeloma U-266
A; Mote: sequence extracted from NCBI backbone (NCBIP:123483)
C; Genetics: CBB:119335; CMIM:147180
A; Grace: CBB:119335; CMIM:147180
A; Map position: 14q32.33-14q32.33
A; Introns: 1/1, 1047, 211/1, 319/1
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C; Complex: An immunoglobulin heterotetron; glycoprotein; heterotetramer; immunoglobulin homology < IMIX>
F; 22-87/Domain: immunoglobulin homology < IMIX>
F; 22-87/Domain: immunoglobulin homology < IMIX>
F; 23-407/Domain: immunoglobulin homology < IMIX>
F; 33-407/Domain: immunoglobulin homology < IMIX>
F; 14/Disulfide bonds: interchain (to light chain) #status predicted
F; 15-105, 29-85, 135-193, 239-259, 345-405/Disulfide bonds: #status predicted
F; 121, 209/Disulfide bonds: interchain (to heavy chain) #status predicted
A;Residues: 'GAWTL',6,'X',8-16,'B',18-43,'B',45-52,55-92,95-97,'B',99-121,'B',123,'L',12
A;Cross-references: UNIPARC:UP10000173785
A;Experimental source: myeloma protona prot
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A,Status: nucleic acid sequence not shown
A,Molecus: nucleic acid sequence not shown
A,Molecus: 98-32 - MRA
A,Residues: 98-35 - KIKE-
A,Cross-references: UNIPARC:UPI0000173788
R,Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.
J. Biol. Chem. 269, 456-462, 1994
A,Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces
A,Reference number: A53116; MUID:94103254; PMID:8276835
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A.Reference number: A46536; MUID:93122085; PMID:8419166
A.Reference number: A6536
A.Residus: preliminary; not compared with conceptual translation
A.Residus: 382-426 *HELD:
A.Residus: 382-426 *HELD:
A.Residus: 382-426 *HELD:
A.Residus: 382-437 *HELD:
A.Residus: 382-331 *HED:
A.Residus: 382-331 *HEZ:
A.Residus: 382-331 *H
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 320-428 <2H2>
A;Cross-references: UNIPARC:UPI000014452D
A;Cross-references: Wyeloma U266-derived cell line AF-10
A;Note: sequence extracted from NCBI backbone (NCBIN:141701, NCBIP:141702)
B;Hellman, L.
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A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-40;68-114;427-428 <KEN>
A;Cross-references: UNIPARC:UPI00001592FD;
R;Ikeyama, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEBS Lett. 224, 306-310, 1987
A,Title: Purification and characterization
A,Reference number: S02438; MUID:88083554;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE 168
                                                                                                                                                     GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD 120
                                                                                                                                                                            169 GELASTOSELTLSOKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD 228
                                                                                                                                                                                                                               LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT 180
                                                                                                                                                                                                                                                     229 LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT 288
                                                                                                                                                                                                                                                                                                        RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
                                                                                                                                                                                                                                                                                                                                                                                 NEMPEDISVOWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV 300
                                                                                                                                                                                                                                                                                                                                                                                                                    408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CiSpecies: Pan troglodytes (chimpañzee)
CiDate: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167 GELASTQSELTLSQKHVLSDRTYTCQVTYQGGTFEDSTKKCADSNPRGVSAYLSRPSPFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEMPEDISVQMLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Introns: 103/1; 209/1; 317/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;336-405/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
   Length
                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Pred. No. 9.6e-115;
3; Mismatches 5;
; Score 1707; DB 1;
; Pred. No. 2.2e-119;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (fragment)
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A; Molecule type: mRNA
A; Residues: 1-388 <LIU>
A; Residues: 1-388 <LIU>
A; Crops-references: UNIPROT: P06336; UNIPARC: UPI000011488C; GB:J00476; NID:g194875; PIDM!
A; Crops-references: UNIPROT: P06336; UNIPARC: UPI000011488C; GB:J00476; NID:g194875; PIDM!
C; Complex: An immunoglobulin nemer subunit consists of two identical light (kapl
hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la
c; Superfamily: immunoglobulin c region; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heteroreteramer; immunoglobulin homology <IM3>
F;186-254/Domain: immunoglobulin homology <IM3>
F;290-361/Domain: immunoglobulin homology <IM4>
F;10,51,62,133,205,228,332,382/Binding site: carbohydrate (Asn) (covalent) #status predl'
                        C;Accession: A02144
R;Liu, F.T.; Albrandt, K.; Sutcliffe, J.G.; Katz, D.H.
Proc. Natl. Acad. Sci. U.S.A. 79, 7852-7856, 1982
A;Title: Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain cDNA.
A;Reference number: A02144; MUID:83117774; PMID:6818553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 TEPTLELLHSSCDPNA-FHSTIQLYCFIYGHILNDVSVSWLMDDREITDTLAQTVLIKEE 122
13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 TPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWL-EDGQVMDVDLSTASTTQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

44.0%; Score 751; DB 1; Length 388;
Best Local Similarity 45.8%; Pred. No. 2e-48;
Matches 147; Conservative 59; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S38864
                                                                                                                                                                                                                  A; Accession: A02144
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Gepsilon chain C region - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 09-Jul-2004

C;Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 09-Jul-2004

C;Accession: A9342; A00937; A02143

R;Hellman, L.; Pettersenon, U; Engstrom, A.; Karlsson, T.; Bennich, H.

Nucleic Acids Res. 10, 6041-6049, 1982

A;Title: Structure and evolution of the heavy chain from rat immunoglobulin E.

A;Recession: A9342;

A;Reserven umber: A93442; MUID:83064537; PMID:622865

A;Reservence: umber: A93442; MUID:8316293; PMID:622865

A;Resperimental source: strain. LOU/c/Wel, immunoglobulin epsilon heavy chain: construction, impactions and immunoglobulin epsilon heavy chain: construction, impactions and immunoglobulin heavy chain: construction, impactions and immunoglobulin heterotetramer subunit consists of two identical light (kappacted)

A;Contents: Myeloma IR162

A;Molecule type: mRNA

A;Reference number: A90937; MUID:83182019; PMID:820340

A;Contents: Myeloma IR162

A;Molecule type: mRNA

A;Residues: Wijstone cases; such as 19A and 19M, the subunits associate into 18

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappacted); immunoglobulin heterotetramer; immunoglobulin homology < IM2>

A;Complex: An immunoglobulin homology < IM2>

F;118-186/Domain: immunoglobulin homology < IM3>

F;123-291/Domain: immunoglobulin homology < IM3>

F;232-391/Domain: immunoglobulin homology < IM3>

F;232-391/Domain: immunoglobulin homology < IM3>

F;232-391/Domain: immunoglobulin homology < IM3>

F;246,99,170,240,265,369,419/Binding site: carbohydrate (Asn) (covalent) # F;46,99,170,240,265,369,419/Binding site: carbohydrate (Asn) (covalent) # F;46,99,170,240,265,369,419/Binding site: carbohydrate Response to the subunit carbohydrate Response to the subun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSG--FFVFSRLEVTRAEWEQKDEFICR 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 TPPTVKILQSSCDGGGHPPPTIQLLCLVSGYTPGTINITWL-EDGQVMDVDLSTASTTQE
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Best Local Similarity 47.4%; Pred. No. 1.7e-51;
Matches 152; Conservative 54; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           299 AVHEAASPSQTVQRAVSVNPG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :||| : ::| : | : | 398 VIHEALREPRKLERTISKSLG 418
                                                                                  407 HEAASPSQTVQRTVSVNPGK 426
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A;Status: preliminary
A;Molecule type: mRWA
A;Residues: 1-548 «KIP»
A;Cross-references: UNIPARC:UP100001165CC; EMBL:Z27397; NID:g416537; PIDN:CAA81788.1; P<sup>‡</sup>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;353-421/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, November 1993
A; Description: Combination of a defined specificity and desired isotype by cloning of
A; Reference number: S38864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŝ
                                                                                                                                                                                                    RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
                                                                                                                                                                                                                                 GELASTOSELTLSOKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD 120
                                                   182
                                                                                                     LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT 180
                                                                                                                                                      241
                                                                                                                                                                                                                                                                                                    NEMPEDISVOWLHNEVQLPDARHSTTQPRKTKGS--GFFVFSRLEVTRAEWEQKDEFICR 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.Species: Mus musculus (house mouse)
C.Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-May-2001
C.Accession: S38864
R.Kipp, B.; Becker, W.; Schlaak, M.
                               |: :| :||||||| | ||:||:
183 LYQNGAPKLTCLVVDLESEK-NVNVTWNQEKKTSVSASQWYTKHNNATTSITSILPVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --TIQLLCLVSGYTPGTINITWL-EDGQVMDVDLSTASTTQEGELASTQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.9%; Score 716; DB 2;
45.0%; Pred. No. 1.2e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig epsilon chain C region - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                         299 AVHEAASPSQTVQRAVSVNPG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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Best Local 5
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- mouse (fragment)

Ig epsilon chain C region (version 1) C; Species: Mus musculus (house mouse)

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J. Exp. Med. 176, 233-243, 1992
A; Title: Two unusual forms of human immunoglobulin B encoded by alternative RNA splicing A; Title: Two unusual forms of human immunoglobulin B encoded by alternative RNA splicing A; Reference number: PH1214; MUID:92308839; PMID:1613458
A; Accession: PH1215
A; Molecule type: DNA
A; Residues: 1-227 < ZHA>
A; Cross-references: UNIPARC:UPI0000176EPC; EMBL:X63693
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig epsilon chain C region form 3 - human (fragment)

N;Alternate names: Ig epsilon chain C region, membrane-bound form (clone CH4-M2')

N;Alternate names: Ig epsilon chain C region, membrane-bound form (clone CH4-M2')

C;Species: Homo sapiens (man)

C;Species: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000

C;Accession: PH1216; D53116

C;Accession: PH1216; D53116

A;Accession: PH1216; D53116

A;Accession: PH1214; May B.E.

A;Attle: Two unusual forms of human immunoglobulin E encoded by alternative RNA splicing

A;Reference number: PH1214; MUID:92308839; PMID:1613458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: PH1216
A;Molecule type: DNA
A;Molecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Cross.references: UNIPARC:UD10000176EFD; EMBL:X63693
A;Cross.references: UNIPARC:UD10000176EFD; A. Saxon, A.
Biol. Chem. 269, 456-462, 1994
A;Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produced
A;Reference number: A53116; MUID:94103254; PMID:8276835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Experimental source: myeloma U266-derived cell line AF-10
A;Note: sequence extracted from NCBI backbone (NCBIN:141701, NCBIN:141711, NCBIP:141718)
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   346 WLGDGKLISNSQHSTTTPLKSNGSNQGFFIFSRLEVAKTLWTQRKQFTCQVIHEALQKPR 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 PRAAPEVYAFATPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKT 60
                                                                                                                                                                                                                                                                                                 C;Spēcies: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 PRAAPEVYAFATPEWPGSRDKRTLACLIONFMPEDISVOWLHNEVQLPDARHSTTQPRKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aintrons: 108/1; 200/3
Cisuperfanily: immunoglobulin C region; immunoglobulin homology
Cikeywords: alternative splicing; immunoglobulin
F;19-88/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272 KGSGFFVFSRLEVTRAEWEQKDEFICRAVHEAASPSQTVQRAVSVNPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.7%; Score 576; DB 2; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                  Ig epsilon chain C region form 2 - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ilarity 100.0%; Pred. No. 1.1
Conservative 0; Mismatches
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A,Residues: 1-243 <ZH2>
A,Cross.references: UNIPARC:UP10000176EFD
                                                                                                                                                                                                                                                                                                                                                        C; Accession: PH1215
R; Zhang, K.; Saxon, A.; Max, E.E.
                                                                                                  ::::| : | 406 KLEKTISTSLG 416
                                                             309 TVQRAVSVNPG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 108; Conserv
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A; Molecule type: DNA
A; Readlades: 1-423 acids
A; Recession: A02145
A; Readlades: 1-423 acids
A; Readlades: 1-423 acids
A; Readlades: 1-423 acids
A; Readlades: 1-423 acids
A; Note: the sequence was determined from the germline gene
C; Genetics:
A; Introns: 91/1; 199/1; 307/1
C; Genetics:
A; Introns: 91/1; immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: In some cases; such as IgA and IgM, the subunits associate into la C; Complex: An immunoglobulin heterotetramer; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F; 16-77/Domain: immunoglobulin homology alWM1>
F; 115-183/Domain: immunoglobulin homology alWM2>
F; 225-396/Domain: immunoglobulin homology alWM3>
F; 225-396/Domain: immunoglobulin homology alWM3>
F; 225-396/Domain: immunoglobulin homology alWM4>
F; 225-396/Domain: immunoglobulin bomology alWM4>
F; 23-75, 122-181, 227-286, 332-394/Disulfide bonds: #status predicted
F; 43, 84, 167, 239, 262, 417/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            epsilon gene: comparison wi
                                                                                                  168 ITEQQWMSESTFTCRVTSQGVDYLAHTRRCPDHEPRGAITYLIPPSPLDLYQNGAPKLIC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          287 VVDRPDFPKPIVRSITILPQVSQRSAPEVYVFPPPE-EESEDKRTLTCLIQNFFPEDISVQ 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WLHNEVQLPDARHSTTQPRKTKGS--GFFVFSRLEVTRAEWEQKDEFICRAVHEAASPSQ 308
                                                                                                                                                                               ITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGTRDWIEGET 188
                                                                                                                                                                                                                                                                                                 YOCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIONFMPEDIS 248
                                                                                                                                                                                                                                                                                                                                                                                                                   VOWLHNEVOLPDARHSTTOPRKTKGS--GFFVFSRLEVTRAEWEOKDEFICRAVHEAASP 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGTRDWIEGETYQC 191
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338 FPPKPKDVLTRSTIQLYCFIYGHILNDVSVSWLMDDREITDTLAQTVLIKEEGKLASTCS 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71
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Ig epailon chain C region (version 2) - mouse
C;Species: Mus musculus (house mouse)
C;Dace: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C;Accession: A02145
R;Ishida, N.; Ueda, S.; Hayashida, H.; Miyata, T.; Honjo, T.
BMBO J. 1, 1117-1123, 1982
BMBO J. 1, 1117-1123, 1982
A;Title: The nucleotide sequence of the mouse immunoglobulin epsilon gene: characterice number: A90966; MUID:84236092; PMID:6329728
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536 PRKLEKTISTS 546
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61 GE-LASTQSELTLSQKHWLSDRTYTCQVTYQGHT--FEDSTKKCADS-NPRGVSAYLSRP 116
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                                                                                                                                   YLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLT 171
                                                                                                                                                                                                                                                                                                                                                           172 VTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRD 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PID:962421
                                                                                                 GELAS----TOSELTLSQKHWLSDRTYTCQVTY--QGHTFEDSTKKCADSNPRG---VSA 111
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                                                                                                                                                                                                                                                                286 NITKNEWERGDEFTCKVKGFPLEPPPLSRSVSKPTGRSFAPTWYVFAPHEMELANYDFVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KRTLACLIQNEMPEDISVQWLHNEVQLPDARHSTTQP-RKTKGSG-FFVFSRLEVTRAEW
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31.0%; Pred. No. 1.7e-27;
ive 72; Mismatches 137; Indels 18;
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Matches 102; Conservative
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A;Molecule type: mRNA
A;Residues: 1-433 <FEL>
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E53116
Ig epsilon chain C region, secreted splice form (clone CH4-3'UT-CH5-M2'') - human (fragm C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: E53116
R;Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.
J. Biol. Chem. 269, 456-462, 1994
A;Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces A;Reference number: A53116; MUID:94103254; PMID:8276835
A;Accession: E53116
A;Accession: E53116
A;Accession: E53116
A;Accession: E53116
A;Accession: E53116
A;Accession: E53116
A;Catus: preliminary
A;Molecule type: DNA
A;Residues: 1-115 <2HA
A;Residues: UNIPARC:UPI000176EFF
A;Experimental source: myeloma U266-derived cell line AF-10
A;Note: sequence extracted from NCBI backbone (NCBIN:141711, NCBIP:141720)
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin homology <IMM>
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B46529
Ig Y heavy chain (7.88) - duck
Ig Y heavy chain (7.88) - duck
N;Alternate names: Ig gamma chain (7.88)
C;Species: Anas platyrhynchos (domestic duck)
C;Species: Auna:1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: B46529; S20759
R;Magor, K.E.; Warr, G.W.; Middleton, D.; Wilson, M.R.; Higgins, D.A.
J. Immunol. 149, 2627-2633, 1992
A;Title: Structural relationship between the two IgY of the duck, Anas platyrhynchos: mc
A;Reference number: A46529; MUID:93017865; PMID:1401901
A;Recession: B46529
A;Status: preliminary
A;Molecule type: mRNA
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-572 *MAG>
A;Coss-references: UNIPARC:UPI0000116038; EMBL:X65219; NID:962442; PIDN:CAA46322.1; PIL
A;Coss-references: UNIPARC:UPI0000116038; EMBL:X65219; NID:962442; PIDN:CAA46322.1; PIL
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Reywords: immunoglobulin homology <IMM>
F;37-120/Domain: immunoglobulin homology <IMM>
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                                                                                                           212 PRAAPEVYAFATPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKT 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                    1 PRAAPEVYAFATPEWPGSRDKRTLACLIQNFWPEDISVQWLHNBVQLPDARHSTTQPRKT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 PRAAPEVYAFATPEWPGSRDKWTLACLIQNFWPEDISVQWLHNEVQLPDARHSTTQPRKT
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                                                                                                                                                                                                                                        272 KGSGFFVFSRLEVTRAEWEQKDEFICRAVHEAASPSQTVQRAVSVNPG 319
                                                                                                                                                                                                                                                                             KGSGFFVFSRLEVTRAEWEQKDEFICRAVHEAASPSQTVQRAVSVNPG 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.6%; Score 471; DB 2; Length 572; 32.0%; Pred. No. 2e-27; Live 66; Mismatches 141; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 570; DB 2; Lengtn ...; Pred. No. 1.38-35;
                                               Indels
                No. 1.2e-35;
natches 0;
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100.0%; Pred. No. 1...
0; Mismatches
                                               Mismatches
                    Pred.
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                    100.0%;
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                                                  108; Conservative
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                Best Local Similarity
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Matches 107;
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212

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272 61 285

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Ig mu chain C region, secreted form - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Oct-1980 #sequence_revision 31-Oct-1980 #text_change 09-Jul-2004
C;Accession: A00166; A26529; A26529; A26240; B02039
R;Kawakami, T.; Takahashi, N.; Honjo, T.
Rviele: Cancies es. 8, 3933-3945, 1980
A;Title: Complete nucleotide sequence of mouse immunoglobulin mu gene and comparison with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1.455 < RAM>
A; Rodeberg, G.I.; Vanin, E.F.; Zrolka, A.M.; Blattner, F.R.
Gene 15, 33-42, 1981
A; Title: Sequence of the gene for the constant region of the mu chain of Balb/c mouse imml
A; Reference number: A26239; MUID:82051295; PMID:6795090
A; Rodecule type: DNA
A; Residues: 1.455 < GOL
A; Rosidues: 1.455 < GOL
A; Rosidues: Unit Ram C: Rougeon, F.
Gene 12, 77-86, 1980
A; Note: the sequence was determined from the germline gene
R; Auffray, C.; Rougeon, F.
Gene 12, 77-86, 1980
A; Rotlectide sequence of a cloned cDNA corresponding to secreted mu chain of mouse
A; Reference number: A26240; MUID:81165562; PMID:6260591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Complete amino acid sequence of a mouse mu chain: homology among heavy chain cot A;Reference number: A02039; MUID:83075344; PMID:6816276
A;Contents: WOPC 104E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: B02039
A;Molecule type: protein
A;Residues: 1-77, 'N',79-100,'Q',102-225,'N',227-257,'T',259-367,'K',369-455 <KEH>
         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      414 GDWENKKQFNCKVVHPDLPSPIEKSIQKSQDPGTEPTITLLPPSDDELRNDFISLICMLK 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                533
                                                                                                                                                                                 63 LASTQSELTLSQKHWLSDRTYTCQVTY-QGHT-FEDSTKKCADSNPRGVSAYLSRPSPFD 120
                                                                                                                                                                                                                                                                                                           121 LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                 181 RDWIEGETYOCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
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                                                                    62
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                                                                                                                            240 PTVEILQGPCASS----KSVELLCLITGYAPSEIKVHWLLNGQVTNISPSNSKPCKEENG
         15; Gaps
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A, Molecule type: mRNA
A, Residues: 1-25, W', 227-257, 'S', 259-367, 'K', 369-455 < AUF>
A, Cross-references: UNIPARC: UP100001737BA
A, Krbiry, M., Sibley, C.; Fuhrman, J.; Schilling, J.; Hood, I
Proc. Natl. acad. Sci. U.S.A. 76, 2932-2936, 1979
A, Reference number: A26241; MUID: 79223904; PMID:111247
         60; Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300 VHEAASPSQTVQRAVSVNPGK 320
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         106; Conservative
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         Matches
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NyAlternate names: Ig nu chain
CiSpecies: Gallus gallus (chicken)
CjDate: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jan-2000
CjAccession: 800390
KiParvari, R.; Avivi, A.; Lentner, F.; Ziv, E.; Tel-Or, S.; Burstein, Y.; Schechter, I.
EMBO J. 7, 739-744, 1988
A;Title: Chicken immunoglobulin gamma-heavy chains: limited VH gene repertoire, combinat
A;Reference number: 800390; MUD:88283642; PMID:3135182
A;Accession: 800390
A;Molecule type: mRNA
A;Residues: 1-504 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Igheavy chain precursor - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 26-Aug-1999
C;Accession: S04845; S05695
R;Ameniya, C.T.; Haire, R.N.; Litman, G.W.
Nucleic Acids Res. 17, 5388, 1989
A;Title: Nucleotide sequence of a cDNA encoding a third distinct Xenopus immunoglobulin A;Reference number: S04845; MUID:89345103; PMID:2503814
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A; Residues: 'LC', 3-308,'H', 310-549 <LIT>
A; Residues: 'LC', 3-308,'H', 310-549 <LIT>
A; Cross-references: UNIPARC:UP10000115E27; EMBL:X15114; NID:964799; PID:9763031
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: glycoprotein; heterotetramer; immunoglobulin
F; 26-109/Domain: immunoglobulin homology <IMM>
F; 26-109/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPGELYISLDAKLRCLVVNL-PSDSSLSVTWTREKSGNLRPDPMVLQEHFNGTYSASSAV 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||::|||||:|||||::||| CLVRGFRPRDIEIRWLRDHRAVPATEFVTTAVLPEERTANGAGGGDTFFVYSKMSVETA 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEVOVLHASSCTPSQ--SESVELLCLVTGFSPASAEVEWLVDGVGGLLVASQSPAVRSGS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLIQNFMPEDISVQWLHNEVQLPDARHSTT----QPRKTKGSG----FFVFSRLEVTRA 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYSLSSRVNVSGTDWREGKSYSCRVRHPATNTVVEDHVKGCPDGAQSCSP--IQLYAIPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 504;
                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPARC:UPI0000176F2A; EMBL:X07174
A;Note: this sequence was determined from the differentiated ger
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 27.5%; Score 469; DB 2; Length 50 Best Local Similarity 32.4%; Pred. No. 2.5e-27; Matches 108; Conservative 60; Mismatches 143; Indels
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A;Residues: 1-549 <AME>
A;Cross-terences: UNIPARC:UPI0000176F30; EMBL:X15114
R;Lituman, G.W.
submitted to the EMBL Data Library, April 1989
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Pred. No. 2.7e-26;
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33.0%;
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A;Accession: S05695
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Best Local Similarity
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             A;Cross-references: UNIPARC:UPI00001737BB
C;Genetics:
A;Introns: 1/1; 106/1; 219/1; 325/1
C;Genetics:
A;Introns: 1/1; 106/1; 219/1; 325/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap C;Complex: An immunoglobulin heterotetramer subunit sasociate into la C;Complex: An immunoglobulin c region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin homology <IMM1>
F;21-91/Domain: immunoglobulin homology <IMM2>
F;23-201/Domain: immunoglobulin homology <IMM3>
F;346-417/Domain: immunoglobulin homology <IMM3>
F;346-417/Domain: carboxyl-terminal <CTS>
F;34-417/Domain: carboxyl-terminal <CTS>
F;147/Disulfide bonds: interchain (to light chain) #status predicted
F;28-89/Disulfide bonds: atte: carbohydrate (Asn) (covalent) #status experimental
F;45-199,246-305,353-415/Disulfide bonds: #status predicted
F;216,454/Disulfide bonds: interchain (to heavy chain) #status predicted
F;293/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A24976
19 mu chain C region (allele b) - mouse
19 mu chain C region (allele b) - mouse
19 mu chain C region (allele b) - mouse
19 c;Species: Mus musculus (house mouse)
2;Species: Mus musculus (house mouse)
2;Daccession: A24976
R;Schreier, P.H.; Quester, S.; Bothwell, A.
Nucleic, Azida Res. 14, 2381-2389, 1986
A;Title: Allotypic differences in murine mu-genes.
A;Reference number: A24976
A;Rolecule type: mRNA
A;References: UNIPARC:UPI0000115D47; GB:X03690; NID:G52381; PIDN:CAA27326.1; PID:GA;Rolecule type: mRNA
A;Residues: 1-455 <SCH>
A;Residues: 1-455 <SCH>
A;Residues: 1-455 <SCH>
C;Resperimental source: strain C57BL/6
A;Note: the authors translated the codon AAG for residue 65 as Leu
C;Superifamily: immunoglobulin C region; immunoglobulin homology
C;Reywords: immunoglobulin homology <IMM>
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32.3%; Pred. No. 3.4e-25;
tive 57; Mismatches 152; Indels
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Best Local Similarity 32.3$
Matches 106; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein November 30, 2005, 00:43:39; Search time 176.232 Seconds (without alignments) 1281.091 Million cell updates/sec Run on:

US-09-847-208B-6 1707 1 FTPPTVKILQSSCDGGGHPP......HEAASPSQTVQRAVSVNPGK 320 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 segs, 705528306 residues Searched: 2166443 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		d			SUMMAKIES	
Result		ouery				
No.	Score		Length	DB	ID	Description
	1707	100.0	428	-	IGHE HUMAN	P01854 homo sapien
8	793	46.5	429	Н	IGHE_RAT	P01855 rattus norv
٣	751	44.0		Н	IGHE_MOUSE	_
4	459.5	26.9	260	~	Q4V801 XENLA	
ū	448.5	26.3	337	7	Q95M34 HORSE	ednn
9	439.5	25.7	454	-	MUC MOUSE	mus
7	439.5	25.7	290	7	Q4V9V8 MOUSE	Q4v9v8 mus musculu
8	434.5	25.5	617	7	Q4KML5 MOUSE	mus
6		25.3	614	7	Q7TMT6 MOUSE	Q7tmt6 mus musculu
10	430.5	25.2	475	7	MUCH MOUSE	mus
11	430.5	25.2	613	~	Q8VCX7 MOUSE	mus
12	430.5		919	~	Q504M7_MOUSE	Q504m7 mus musculu
13	426	25.0	464	~	Q6MZU6_HUMAN	_
14	423.5	24.8		7	MUC_MESAU	P06337 mesocricetu
15	421	24.7	465	N	Q6P6C4 HUMAN	рошо
16	420	24.6		~	Q6N093_HUMAN	homo
17	417	24.4	470	~	Q68CN4 HUMAN	homo
18	416	24.4	326	-	IGHG2 HUMAN	homo
19	414	24.3	458	~	Q652Q1 HUMAN	homo
20	413.5	24.2		Н	MUC SUNMU	Bunch
21	413	•		~	Q86TT1 HUMAN	_
22	413	24.2		~	Q99LC4_MOUSE	mus m
23	413			7	Q9BU10 HUMAN	homo
24	413			7	Q9BQB8 HUMAN	homo
25	413			7	Q96BB9_HUMAN	homo
56	413			~	Q6GMX5_HUMAN	рошо
27	413			7	Q6GMY2_HUMAN	homo
28	410.5	24.0		~	QSRK07 RAT	Q5rk07 rattus norv
29	410.5	24.0		~	1	Q569b8 rattus norv
30	410.5	24.0	591	7	QSIOL9 RAT	Q5i019 rattus norv
31	410.5	24.0	591	7	Q4QQW0_RAT	Q4qqw0 rattus norv

Q568y0 rattus norv P04220 homo sapien P01871 homo sapien P0188 oryctolagus P01862 cavia porce Q6pf95 mus musculu Q6n089 homo sapien Q8wux1 homo sapien Q96ey0 homo sapien P01868 mus musculu Q6pjb8 mus musculu Q6pjb2 mus musculu
Q568Y0 RAT MUCE HIMAN MUC HUMAN MUC TABIT I GHG2 CAVPO Q6PP95_MOUSE Q6NUS HUMAN Q98WUX-HUMAN Q96XY0 HUMAN Q96AAG HUMAN Q96AAG HUMAN G96AAG HUMAN G96AAG HUMAN G96AAG HUMAN
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ALIGNMENTS

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                                                                                                             This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                               MEDLINE=87089848; PubMed=3796618; DOI=10.1016/0161-5890(86)90005-2; Padlan E.A., Davies D.R.; Padlan E.A., Davies D.R.; Model of the Fc of immunoglobulin E."; Mol. Immunol. 23:1063-1075(1986).
ımmunoglobulin epsilon chain expressed in a myeloma cell line.";
Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
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#### PROSITE; PS08093; IG_LIKE; 4.

#### PROSITE; PS08093; IG_LIKE; 4.

#### PROSITE; PS08093; IG_MHC, 3.

#### PROSITE; PS08093; IG_NHC, 3.

#### PROMAIN 112 210 IG_like 3.

#### PT DOWAIN 214 318 IG_like 3.

### PT DOWAIN 324 423 IG_like 3.

#### PT CARBOHYD 21 21 N-linked (GICNAC. .).

#### PT CARBOHYD 49 99 N-linked (GICNAC. .).

#### PT PROSITE; PS08093; IG_NHC, IG
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/FTId=VAR 003885.
                                                                                                                                                                                           EMBL; L000022; AABS9424.1; ALT_INIT; Genomic_DNA.
PIR; A22771; EHHU.
PDB; 1F6A; X-ray; BD=211-428.
PDB; 1FF5; X-ray; A=211-428.
PDB; 1GB; Model; A/B=106-208.
PDB; 1IGE; Model; A/B=107-428.
PDB; 1IGE; Model; A/B=107-428.
PDB; 1OVY; X-ray; A/B=106-427.
Ensembl; ENSG0000177154; Homo sapiens.
HGNC; HGNC:5522; IGHE.
MIM; 147180; -
GO; GO:0008923; F:antigen binding; NAS.
GO; GO:0008923; F:antigen binding; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003004; Ig-c1.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00647; Ig: 1.
PFM MAN.
PFM MAN.
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                                                                                                                                                                                                                                                                                                                                     Match 100.0%; Score 1707; DB 1; Local Similarity 100.0%; Pred. No. 1.5e-128; es 320; Conservative 0; Mismatches 0;
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NEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSG--FFVFSRLEVTRAEWEQKDEFICR 298
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Ensembl; ENSMUSGO000021153; Mus musculus.
InterPro; IPR00710; Ig-like.
InterPro; IPR00710; Ig-Li.
InterPro; IPR003006; Ig-MHC.
Pfam; PF07654; Cl-Bet; I.
Pfam; PF07654; Cl-Bet; I.
PRART; SW00407; IGG1; 2.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 3.
                                                                                                                     421 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X01857; CAA25977.1; -; Genomic_DNA.
EMBL; X01857; CAA25978.1; -; Genomic_DNA.
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                                           299 AVHEAASPSQTVQRAVSVNPG 319
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PIR; A02145; EHMSS.
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                                                      Hellman L., Pettersson U., Engstroem A., Karlsson T., Bennich H., "Structure and evolution of the heavy chain from rat immunoglobulin
                                                                                                                                                                                     NUCLEOTIDE SEQUENCE OF 205-306.

MEDLINE-BAIT45/6. PubMed-6803238.

Hellman L., Pettersson U., Bennich H.;

"Characterization and molecular cloning of the mRNA for the heavy
"Characterization of rat immunoglobulin E.",

Proc. Natl. Acad. Sci. U.S. A. 79:1264-1268(1982).

-: SIMILARITY: Contains 4 Ig-like (immunoglobulin-like) domains.
                                                                                                                 MEDLINE=83182019; PubMed=6820340; Kindsvogel W.R., Reddy E.P., Moore J.M., Faust C.H. Jr.; "A cloned cDMA probe for rat immunoglobulin epsilon heavy chain: construction, identification, and DNA sequence."; DNA 1:335-343(1982).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.5%; Score 793; DB 1; Length 429; 47.4%; Pred. No. 3.7e-55;
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Ensembl; ENSRNOG0000005328; Rattus norvegicus.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003367; Ig-c1.
InterPro; IPR003306; Ig-Mic.
Pfam; PF07654; C1-set; Z.
Pfam; PF07654; C1-set; Z.
SMART; SM00407; IGc1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_LIKE; 4.
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Ig-like 2.
Ig-like 3.
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R -> N (in Ref. 2).
P -> L (in Ref. 2).
                                                                                                             NUCLEOTIDE SEQUENCE OF 168-342 (MYELOMA IR162).
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PIR; A93442; EHRT.
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                         NUCLEOTIDE SEQUENCE (IMMUNOCYTOMA IR2)
                                                                                        Nucleic Acids Res. 10:6041-6049(1982)
                                               MEDLINE=83064537; PubMed=6292865;
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NUCLECTIDE SEQUENCE OF 34-421.
MEDIJNE-83117774; PubMed-6818553;
Liu F.-T., Albrandt K., Sutcliffe J.G., Katz D.H.;
"Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain
                                                                                                                                                                                                                                                                                          po6335, po1856; 21-JUL-1986 (Rel. 01, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
1g epsilon chain C region.
Mus musculus (Mouse).
Eukaryota, Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontcolires; Glires; Rodentia; Sciurognathi;
Murcoidea; Muridae; Murinae; Mus.
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NUCLOTIDE SEQUENCE.
NUCLINE=84236092; PubMed=6329728;
Ishida N., Ueda S., Hayashida H., Miyata T., Honjo T.;
Ishida N., Locia Sequence of the mouse immunoglobulin epsilon gene:
"The nucleotide sequence of the mouse is immunoglobulin epsilon gene:
comparison with the human epsilon gene sequence.";
EMBO J. 1:1117-1123(1982).
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Submitted (APR-1986) to the EMBL/GenBank/DDBJ databases
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                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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 (Potential). (Potential).
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                                                                                                                     9
                                                                                               Length 421;
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                                                                                            44.0%; Score 751; DB 1; Length 42
45.8%; Pred. No. 8.6e-52;
ive 59; Mismatches 109; Indels
                                                                          47321 MW; 8F909E1F30A06B47 CRC64;
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Last annotation update)
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Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski m. Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
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MEDLINE=98383416; PubMed=9717671;
Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
Leibold W., Radbruch A.;
"Organization of the equine immunoglobulin heavy chain constant region genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
Immunobiology 199:105-118(1998).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
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MEDLINE=22172648; PubMed=12185539; DOI=10.1007/s00251-002-0458-4;
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Immunogobulin gamma 1 heavy chain constant region (Fragment)
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Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BC0976-9; AAH97629.1; -; mRNA.
SEQUENCE 560 AA, 61795 WW; 9DED2DD2B17CFDBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2004 (TrEMBLrel. 26,
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Q95M34;
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107; Conservative
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Gene 15:33-42(1981)
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01-FBB-2005 (Rel. 46, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
1g mu chain C region secreted form.
Mus musculus (Mouse)

Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buzrontoglires; Glires; Rodentia; Sciurognathi;
Murcoidea; Muridae; Musinae; Mus.
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MEDLINE=82051295; PubMed=6795090; DOI=10.1016/0378-1119(81)90102-5; Goldberg G.IL., Vanin B.F., Zrolka A.M., Blattner F.R.; Sequence of the gene for the constant region of the mu chain of Balb/c mouse immunoglobulin.";
Wagner B., Greiser-Wilke I., Wege A.K., Radbruch A., Leibold W.; "Evolution of the six horse IGHG genes and corresponding immunoglobulin gamma heavy chains."; Immunogenetics 54:353-364 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                           25;
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MEDLINE=81076590; PubMed=6255422;
Kawakani T., Takahashi N., Honjo T.;
"Complete nucleotide sequence of mouse immunoglobulin mu gene comparison with other immunoglobulin heavy chain genes.";
Nucleic Acids Res. 8:3933-3945(1980).
                                                                                                                                                                                                                                                                                      immunogobulin gamma 1 heavy chain
                                                                                                                                                                                                                                                                                                                                                                                              26.3%; Score 448.5; DB 2; Length 337; 31.3%; Pred. No. 1.36-27; Live 62; Mismatches 146; Indels 25;
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337 AA; 37438 MW; A60BF2B01DEFDIF6 CRC64;
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                                                                                   EMBL, AJ300675; CAC44624.1; -; mRNA. HSSP; PO1857; 1HZH.
HREPTO; 1PR007110; 1g-11ke.
InterPro; 1PR003597; 1g-21.
InterPro; 1PR003597; 1g-MHC.
Pfan; PF07654; C1-8et.; 3.
SMART; SMO0407; IG-11KE; 3.
PROSITE; PS00230; IG_LIKE; 3.
PROSITE; PS00230; IG_MHC; UNKNOWN 2.
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Matches 106; Conservative
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P01872;
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Enterpoly (2010) (1981); Casternal side of plasma membrane; IDA.

RO; GO: 0019815; C: B cell receptor complex, IDA.

RO; GO: 0019815; C: External side of plasma membrane; IDA.

RO; GO: 0048471; C: perimuclear region; IDA.

RO; GO: 0048471; C: perimuclear region; IDA.

RO; GO: 0004881; F: transmembrane receptor activity; IDA.

RO; GO: 0004888; F: transmembrane regulation of endocytosis; IDA.

RO; GO: 0005885; F: PRO03110; IG-IKE.

RO; GO: 0005885; IG-IKE; A.

RROSITE; RS00290; IG-IKE; A.

RWOSITE; RS00290; IG-IKE; A.

RWOSITE; RS00290; IG-IKE; A.

RWART; RMMO407; RGC1; A.

RWART; RMMO4040; RGCMMO407; RGCMMO407; RGCMMO407; RGCMMO407; RGCMMO407; RGCMMO407; RGCMMO407; RGCMMO407; RGCM
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NUCLEOTIDE SEQUENCE (MYELOMA TEPC183).
MEDLINE-81165562; PubMed-6260591; DOI-10.1016/0378-1119(80)90017-7;
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Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
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                                                                                  Auffray C., Rougeon F.;
"Nucleotide sequence of a cloned cDNA corresponding to secreted chain of mouse immunoglobulin.";
Gene 12:77-86(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  heavy chain constant region domains.";
Biochemistry 21:5415-5424(1982).
-!- SUBCELLULAR LOCATION: Secreted (Probable).
-!- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
Comment-During differentiation, B lymphocytes switch from expression of isoform Membrane-bound to isoform Secreted;
                                                                                                                                                                                                                                                                                                             PROTEIN SEQUENCE (MYELOMA PROTEIN MOPC 104E).
MEDLINE-79223904; PubMed=111247;
KEDLY M.R., Sibley C.H., Fuhrman J.S., Schilling J.W., Hood I Manino acid sequence of a mouse immunoglobulin mu chain.";
Proc. Natl. Acad. Sci. U.S.A. 76:2932-2936(1979).
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EMBL; J00444; AAB59650.1; JOINED; Genomic_DNA.
EMBL; V00827; -; NOT_ANNOTATED_CDS; MRNA.
PIR; A02166; MHMS.
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IsoId=P01872-1; Sequence=Displayed;
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Statchen M., Soares M.B., Bonaldo M.F., Casavant T.I., Scheetz T.E., Rownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McKernan R.J., Malek J.A., Gunzatne P.H., Anderson R.J., Malek J.A., Gunzatne P.H., Anderson R.J., Lu X., Gibbs R.A., Anilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Rahey J., Halton B., Ketteman M., Madan A., Rodrigues S., Sanchez A., Butkesley R.W., Touchman J.W., Green E.D., Dickson M.C., Antingo M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Antingo M., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Topeneration and initial analysis of more than 15,000 full-length human manage of the state of the st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235 LACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGS-GF-FVFSRLEVTRAEWEQK 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 LASTQ----SELTLSQKHWLSDRTYTCQVTYQGHTF-EDSTKKCADSNPRGVSAYLSRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases EMBL, BC096667, AAH96667.1; -; mRNA. MGI:96448; Igh-6.
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590 AA; 64892 MW; D425318F9A188B14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.7%; Score 439.5; DB 2; 32.3%; Pred. No. 1.4e-26; ive 57; Mismatches 152;
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1D Q4KMLS MOUSE PRELIMINARY; PRT; 617 AA.

AC Q4KMLS,

DT 13-5EP-2005 (TrEMBLrel. 31, Created)

DT 13-5EP-2005 (TrEMBLrel. 31, Last sequence update)
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PROSITE; PS00290; IG MHC; UNKNOWN_3.
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Interproj IPR00110; Ig-like.
Interproj IPR00110; Ig-cl.
Interproj IPR003597; Ig_cl.
Interproj IPR003596; Ig_WHC.
Interproj IPR003596; Ig_WHC.
SMART; SM00409; IG; 2.
SMART; SM00407; IGcl; 4.
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TISSUE=Mammary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH MGC Project;
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                                                                                                                                                                                 By similarity.

Interchain (with heavy chain) (Probable).
By similarity.
Interchain (with heavy chain) (Probable).
By similarity.
Interchain (with heavy chain) (Probable).
S -> N (in MOPC 104E).
H -> Q (in MOPC 104E).
T -> N (in TEPC18B).
N -> S (in TEPC18B).
N -> K (in TEPC18B).
L -> K (in TEPC18B).
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          N-linked (GlcNAc. . .).
Interchain (with light chain) (Probable)
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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MEDLINE=22388351; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 requires 2 nucleotide substitutions)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.7%; Score 439.5; DB 1; Length 454; 32.3%; Pred. No. 9.8e-27; ive 57; Mismatches 152; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 454 AA; 49972 MW; EBCCA6E8569AEEC5 CRC64;
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Last annotation update)
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Best Local Similarity 32.3*
Matches 106; Conservative
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Q4V9V8;
                    Mus musculus (Mouse)
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                 Name=Igh-6;
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CARBOHYD
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DQ 4049V8 MO
DD 13-S
DD 13-S
DT 13-S
DD 13-S
DD 13-S
DD MARRO
GN NARRO
GN NARRO
CO MARRO
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                                                                                                                                    STRAIN-C57BL/GNCT; TISSUE-Hematopoietic Stem Cell;

KEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RIJachenko L., Marusina K.H., Farmer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robar S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahet J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length human
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VTCLVKGFSPADISVQWLQRGQLLPQEKYVTSAPMPEPGAPGFYFTHSILTVTEEEWNSG 551
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                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 25.5%; Score 434.5; DB 2; Lengtn Best Local Similarity 32.6%; Pred. No. 3.7e-26; Matches 105; Conservative 54; Mismatches 150; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases. EMBL; BC099504; AAH98504.1; -; mRNA. Hypothetical protein. SEQUENCE 617 AA; 68520 MW; BCF2AEC857CD3D12 CRC64;
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
STRAIN=CS7BL/6NCr; TISSUE=Hematopoietic Stem Cell;
NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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13-SEP-2005 (TrEMBLrel.
             Hypothetical protein.
Mus musculus (Mouse).
                                                                                                                               SEQUENCE
                                                                                               NCBI_TaxID=10090;
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RETAINLE-27BL/GNCT, TISSUE-Hematopoietic Stem Cell;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausherg R.L., Feingold E.A., Grouse L.H., Borge J.G.,

RA Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

Raha S.G., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

R. Admurch A., Schein J.E., Jones S.J.M., Marra M.A.;

R. Admurch A., Schein J.E., Jones S.J.M., Marra M.A.;

R. Admurch A., Schein J.E., Mones E.J.M., Marra M.A.;

R. Admurch A., Schein J.E., Mones E.J.M., Marra M.A.;

R. Admurch A., Schein J.E., Mones B.J.M., Marra M.A.;

R. Admurch A., Schein J.E., Mones B.J.M., Marra M.A.;

R. Admurch A., Schein J.E., Mones B.J.M., Marra M.A.;

R. Admurch A., Schein J.E., Mones B.J.M., Marra M.A.;

R. Admurch A., Schein J.E., Mones B.J.M., Marra M.A.;

R. Admurch A., Schein J.E., Mones B.J.M., Marra M.A.;

R. Admurch A., Schein J.E., Mones B.J.M., Marra M.A.;
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                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        614 AA; 67747 MW; 839BAF3B8D124F89 CRC64;
                                                       Last sequence update)
Last annotation update)
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                                                 01-OCT-2003 (TrEMBLrel. 01-MAR-2004 (TrEMBLrel.
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                                                                                                                                                                     MGC60843 protein.
Mus musculus (Mouse)
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9

614 AA.

PRT:

Q7TMT6 MOUSE PRELIMINARY; Q7TMT6;

MOUSE

RESULT 9
Q7TMT6 MO
ID Q7TM

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QBVCX7
QBVCX7;
QBVCX7;
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2004 (TrEMBLrel. 20,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104; Conservative
                                                                                                                                                                                         domain;
                                                                                                                                                                                                                                                                                                                       13
88
198
215
304
292
                                                                                                                                                                             Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                       475 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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Name=Igh-6;
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TRANSMEM
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Q8VCX7 MOU

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                 LACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGS-GF-FVFSRLEVTRAEWEQK 292
                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=80222873; PubMed=6771019; DOI=10.1016/0092-8674(80)90616-9; Rogers J., Early P., Carter C., Calame K., Bond M., Hood L., Wall R.; Two mRNAs with different 3' ends encode membrane-bound and secreted forms of immunoglobulin mu chain."; Cell 20:303-312(1980).
                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=80222874; PubMed=6771020; DOI=10.1016/0092-8674(80)90617-0; Early P., Rogers J., Davis M., Calame K., Bond M., Wall R., Hood L., Two mRNhs can be produced from a single immunoglobulin mu gene by alternative RNh processing pathways."; Cell 20:313-319(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isold=P01872-1; Sequence=External; MISCELLANEOUS: The sequence of residues 1-409 is assumed to be identical with the corresponding region of the secreted form.
                                                                                                                                                                                                                                                                                                                                   and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=2;
Comment=During differentiation, B lymphocytes switch from
expression of isoform Membrane-bound to isoform Secreted;
                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO:0019815; C:B cell receptor complex; IDA.
GO:000897; C:external side of plasma membrane; IDA.
GO:000897; C:exmunoglobulin complex, circulating; IDA.
GO:0042571; C:immunoglobulin complex, circulating; IDA.
GO:000881; F:antigen binding; IDA.
GO:0004888; F:transmembrane receptor activity; IDA.
GO:0000187; F:activation of MAPK; IDA.
                                                                                                                                                                                                                                                                                                    MEDLINE-81076590; PubMed-6255422;
Kawakami T., Takahashi N., Honjo T.;
"Complete nucleotide sequence of mouse immunoglobulin mu
comparison with other immunoglobulin heavy chain genes.";
Nucleic Acids Res. 8:3933-3945(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE OF 409-475 (MYELOMA MOPC 104E)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; J00443; AAB59651.1; -; Genomic_DNA.
EMBL; J00444; AAB59651.1; JOINED; Genomic_DNA.
EMBL; V00821; CAA24202.1; -; mRNA.
                                                                                                                                                                            01-FEB-2005 (Rel. 46, Last sequence update) 10-MAY-2005 (Rel. 47, Last annotation update) Ig mu chain C region membrane-bound form.
                                                                                                                                        475 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=P01873-1; Sequence=Displayed;
                                                  DEFICRAVHEAASPSQTVQRAV 314
                                                                   ETYTCVVSHEAL-PHLVTERTV 569
                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE OF 432-475
                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=Membrane-bound;
                                                                                                                                        STANDARD;
                                                                                                                                                                                                                  musculus (Mouse).
                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE
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HSSP; P01861; 1ADQ.
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P01873;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231 SFADIFLSKSANLTCLVSNLATYE-TLNISWASQSGEPLETKIKIMESHPNGTFSAKGVA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235 LACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGS-GF-FVFSRLEVTRAEWEQK 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         350 VICLVKGFSPADÍSVQWLQRGQLLPQEKYVTSAPMPEPGAPGFYFTHSILTVTEEEWNSG 409
GO:003033; P:antigen processing; IDA.
GO:005085; P:B cell receptor signaling pathway; IDA.
GO:005085; P:B carly endosome to late endosome transport; IDA.
GO:0016064; P:humoral defense mechanism (sensu Vertebrata); IDA.
GO:0030890; P:postitive regulation of B cell proliferation; IDA.
GO:0045807; P:positive regulation of endocytosis; IDA.
GO:0050731; P:positive regulation of peptidyl-tyrosine ph. . .; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 PTVKILQSSCDG-GGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 SPPDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 PVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATP--EWPGSRDKRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290 SVCVEDWNNRKEFVČTVTHRDLPSPQKKFISKPNEVHKHPPAVYLLPPAREQLNLRESAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interchain (with heavy chain) (Probable) By similarity.
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                                                                                                                                                                                                                                                                                                                                                        Glycoprotein; Immunoglobulin C region; Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52527 MW; F2163AD4517E1485 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GlcNAc. ..).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.2%; Score 430.5; DB 1
32.3%; Pred. No. 5.5e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GlcNAc.
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CH3.
CH4.
N-linked
N-linked
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                                                                                                                                                                     InterPro; IPR007110; Ig-11ke,
InterPro; IPR003597; Ig_c1,
InterPro; IPR003006; Ig_MHC.
Pfam; PF07654; C1-set; 4,
SMART; SM00407; IgG1; 4,
PROSITE; PS50835; IG_LIKE; 4,
PROSITE; PS00290; IG_MHC; 3.
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RGO; G0:0019915; C:B cell receptor complex; IDA.

GO; G0:0009915; C:B cell receptor complex; IDA.

GO; G0:0009915; C:B cell receptor complex; IDA.

GO; G0:00042571; C:immunoglobulin complex, circulating; IDA.

RGO; G0:0004871; C:perinuclear region; IDA.

GO; G0:0004883; F:protein binding; IPI.

RGO; G0:0004888; F:transmembrane receptor activity; IDA.

RGO; G0:000515; P:protein of MAPK activity; IDA.

GO; G0:0005033; P:antigen processing; IDA.

RGO; G0:0005033; P:antigen processing; IDA.

GO; G0:0005033; P:antigen processing; IDA.

RGO; G0:0016064; P:humoral defense mechanism (sensu Vertebrata); IDA.

RGO; G0:0016064; P:humoral defense mechanism (sensu Vertebration; IDA.

RGO; G0:0016064; P:humoral defense mechanism (sensu Vertebrata); IDA.

RGO; G0:0016064; P:humoral defense mechanism (sensu Vertebr
                                                                                                                                                                                                    STRAINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
A Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haite F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haite F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haite F.,
A Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
A Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S. A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
A Willalon D.K., Muzny D.M., Sodergren B.J., Lux, Gibbs R.A.,
A Willalon D.K., Muzny D.M., Garcia A.M., Gay L.J., Hulyk S.W.,
A Willalon D.K., Muzny D.M., Garcia A.M., Gay L.G., Hulyk S.W.,
A Willalon D.K., Muzny D.M., Grenn B.D., Dickson M.C.,
A Blakesley R.W., Touchman J.W., Grenn E.D., Dickson M.C.,
A Butterfield Y.S.N., Krzywinski M.I., Skalska W., Smailus D.E.,
A Schnerch A. Schehul J.E., Jones S.J.M., Marra M.A.;
A Cheneration and initial analysis of more than 15,000 full-length human
The Froc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=2464031;
Sikder S. K., Borden P., Gruezo F., Akolkar P.N., Bhattacharya S.B.,
Mortzhon S.L., Kabat E.A.;
Maritson S.L., Kabat E.A.;
"Amino acid substitutions in VH CDR2 change the idiotype but not the
antigen-binding of monoclonal antibodies to alpha(1---6)dextrans.";
J. Immunol. 142:888-893(1889).
BMBL; BC018315; AAH18315.1; -; mRNA.
BTR; C30562; C30562.
HSSP; P01751; 1A6W.
Ensembl; ENSWUSG00000054328; Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
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PROSITE; PS00290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
STRAIN=FVB/N; TISSUE=Salivary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunoglobulin domain
SEQUENCE 613 AA; 6
                                                                                             Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00406; IGV;
musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                                 NCBI_TaxID=10090;
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RE ROLLINE-22380257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RIBDINE-22380257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Ribour R.E., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Districtancy L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Raha S.S., Logdellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Logdellano N.A., Peters G.J., Abramson R.D., Mullahy S.W.,
Robards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gübbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Whiting M., Madan J.W., Green B.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
R. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                         117 SPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL 176
                                                                                                                                                                                                                                                                                                                                                                                487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGS-GF-FVFSRLEVTRAEWEQK 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177 PVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATP--EWPGSRDKRT
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                               4 PTVKILQSSCDG-GGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGE
Length 613;
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EMBL, BC094936; AAH94936.1; -; mRNA.
InterPro; IPR003599; Ig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
   DB 2;
                                                         56; Mismatches 149;
                              .6e-26
25.2%; Score 430.5; 32.3%; Pred. No. 7.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              548 ETYTCVVGHEAL-PHLVTERTV 568
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                           32.3%;
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Q504M7;
   Query Match
Best Local Similarity 32.3<sup>1</sup>
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
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SMART; SM00406; IGv; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUC MESAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                              165
                                                                                                                               Query Match
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MUC_MESAU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SFADIFLSKSANLTCLVSNLATYE-TLNISWASQSGEPLETKIKIMESHPNGTFSAKGVA 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATP--EWPGSRDKRT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            431 SVCVEDWNNRKEFVCTVTHRDLPSPOKKFISKPNEVHKHPPAAVILLPPAREQLNLKESAT 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGS-GF-FVFSRLEVTRAEWEQK 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                        4 PTVKILQSSCDG-GGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGE
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Bloecker H., Boacher M., Brandt P., Mewes H.W., Weil B., Amid C., A Ganger A., Fobo G., Han M., Wiemann S.; Submitted (JAM-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BX640874; CAE45931.1; -; mRNA.
EMBL; BX640874; CAE45931.1; -; mRNA.
RSSP, PO1861; 1ADQ.
RIDGEPTO; IPR003599; Ig.
RIDGEPTO; IPR003599; Ig.
RIDGEPTO; IPR003599; Ig.
RIDGEPTO; IPR003596; Ig.Cl.
RIDGEPTO; IPR003596; Ig.Cl.
RIDGEPTO; IPR003596; Ig.Cl.
RIDGEPTO; IPR00369; IG.Cl.
RIDGEPTO; IRROBANG; IG.Cl.
RIDGEP
                                                                                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                                                       25.2%; Score 430.5; DB 2; Length 616; 32.3%; Pred. No. 7.7e-26; ive 56; Mismatches 149; Indels 13
                                                                                                                                                                                                         Hypothetical protein.
SEQUENCE 616 AA; 67919 MW; 0FF4532BCD596A52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686C15213.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               464 AA
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003596; Ig_WHC.
InterPro; IPR003596; Ig_V.
Pfam; PF07654; C1-set; 4.
SWART; SW00409; IG; 2.
SWART; SW00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         551 ETYTCVVGHEAL-PHLVTERTV 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE,
TISSUE=Rectum tumor;
The German cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QEMZUG HUMAN PRELIMINARY;
QEMZUG;
                                                                                                                                                                                                                                                                                                               Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=DKFZp686C15213;
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117
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Q6MZU6_HUN
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 -RGVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              312 QFNSTFRVVSVLTVVHQDMLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTL--- 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369 --PPSREEMTKNOVSLTCLVKGFYPSDIAVEWESN--GQPENNYKTTPPMLDSDGSFFLY 424
                                                                                                                                                                                                                                                                                                  6 VKILQSSCDGGGHFP-----PTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA
                                                                                                                                                                                                                                                                                                                                       56 STTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQ-GHTFEDST---KKCADSNP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGMEVHNAKTKPREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225 EWPGSRDKRT----LACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVF
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Cricetidae; Cricetinae; Mesocricetus.
                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                     36;
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InterPro; PR000110; 19-1ike.
InterPro; IPR000110; 19-1ike.
InterPro; IPR000106; 19-1ike.
Pfam; PF07654; C1-set; 4.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00200; IG_MHC; 3.
PROSITE; PS00200; IG_MHC; 3.
REGION I 1005
CH1.
                                                                                                                                                                     Length 464;
                                                                                                                                                              25.0%; Score 426; DB 2; Length 46
31.1%; Pred. No. 1.2e-25;
ive 62; Mismatches 137; Indels
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS0290; IG_MHC; UNKNOWN_2.
Hypotheticlal protein.
SEQUENCE 464 AA; 51099 MW; 2FCA72C66EBAOABC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 SRLEVTRAEWEQKDEFICRAVHEAASPSQTVQRAVSVNPGK 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1988 (Rel. 06, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
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Mesocricetus auratus (Golden hamster).
                                                                                                                                                                                                                                  Matches 106; Conservative
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                                                                                                                                                                                                   Best Local Similarity
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231 SFVGIFLNKSATLTCLVTNLA-TYDTLNISWSSRSGEPLETKTKLTESHPNGTFSAIGEA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LASTQ-----SELTLSQKHWLSDRTYTCQVTYQGHTF-EDSTKKCADSNPRGVSAYLSRP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPR----AAPEVYAFATPEWPGSRDK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284
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Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290 NVCVEDWDSGKEFVCTVTHRDLPSPQKKFISK----PREMNKTPPAVY-----QQPLAREQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTVKILQSSCDG-GGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGE
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                                                                                                                                                                                                                                Interchain (with light chain) (Probable).
By similarity.
By similarity.
Interchain (with heavy chain) (Probable).
                                                                                                                                                                                                                                                                                                                       By similarity.
Interchain (with heavy chain) (Probable)
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Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                         (Potential).
(Potential).
(Potential).
(Potential).
(Potential).
(Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              4DA2134612BE1469 CRC64;
                                                                  (GlcnAc. . . ) (GlcnAc. . . )
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.8%; Score 423.5; DB 1 31.5%; Pred. No. 1.9e-25;
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CH2.
CCH3.
CCH4.
N-linked
N-linked
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QEP6C4_HUMAN PRELIMINARY;
Q6P6C4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 31.5
les 106; Conservative
                                                               445
1112
1192
2210
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4411
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4414
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TISSUE=Spleen;
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NON TER
SEQUENCE
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                                                                                                                                               CARBOHYD
                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                         CARBOHYD
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135 VTVSSASTKGPSVPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW-NSGALTSGVHTFP 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATP 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          313 QFNSTPRVVSVLTVVHQDMLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTL--- 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 EWPGSRDKRT----LACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVF 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramoon R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunartne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Sodergren E.J., Lu K., Gibbs R.A., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Brackfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones J.M., Marra M.A., Schein J.E., Jones J.M., Schein J.E., Jones J.M., Marra M.A., Schein J.E., Jones J.M., J.M., Marra M.A., Schein J.E., J.M., J.M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Strausberg R.; | Strausberg R.; | Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases. | Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases. | EMBL, BCO66235; AAH62335.1; -; mRNA. | HSSP; PO1664; 20-465. | SMR; Q6P6C4; 20-465. | SMR; Q6P6C4; 20-465. | InterPro; IPR001359; Ig. | InterPro; IPR001359; Ig. | InterPro; IPR0013006; Ig_MHC. | InterPro; IPR001306; Ig_MHC. | InterPro; IPR001306; Ig_W. | R SMART; SM00409; IG; 2. | SMART; SM00409; IG; 2. | SMART; SM00406; IGv; 1. | R SMART; SM00406; IGv; 1. | R SMART; SM00406; IG_WC; UNKNOWN_2. | R PROSITE; PS002290; IG_MHC; UNKNOWN_2. | R PROSITE; PS002290; IG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 465;
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31.1%; Pred. No. 3.1e-25;
ive 61; Mismatches 138; Indels
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REQUENCE 465 AA; 51325 MW; FDDB9348ADC37E6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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hes 106; Conservative 6
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Search completed: November 30, 2005, 00:56:33 Job time : 178.232 secs

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ALIGNMENTS

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, OTHER INFORMATION: Synthetically generated proteins US-09-401-636-1
US-09-401-636-1
US-09-401-636-1
Sequence 1, Application US/09401636
Factor No. 6913749
GENERAL INFORMATION:
APPLICANT: Hellman, Lars T.
TITLE OF INVENTION: ENHANCED VACCINES
FILE REFERENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/09/401,636
CURRENT APPLICATION NUMBER: US 60/106,652
FRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 11
SOUTHWARE: FASTERO FOR Windows Version 4.0
SEQ ID NO 1
LENGTH: 331
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ORGANISM: Artificial Sequence
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ö 191 GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD 120 LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT 180 RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240 192 RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 251 9 7 12 FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTAGE FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE Gaps ö Length 331; 0; Indels ; Score 1707; DB 2; ; Pred. No. 3.3e-156; 0; Mismatches 0; 100.0%; Best Local Similarity 100. Matches 320; Conservative

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Sequence 8, Application US/10211948

| Sequence 8 | Application US/10211948 |
| Patent No. 6889145 |
| GENERAL INFORMATION: |
| APPLICANT: Jardedtzky, Theodore S. |
| APPLICANT: Wurzburg, Beth A. |
| TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A FC REGION OF AN IGE ANTIBODY AND USEF |
| TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A FC REGION OF AN IGE ANTIBODY AND USEF |
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                                                                                                                                                                                                                                                                                                                                                                                                                       103 DSNPRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 DSNPRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKE
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                                                                                                                                                                                                                                                                                                         Query Match 67.8%; Score 1158; DB 2; L
Best Local Similarity 100.0%; Pred. No. 1.6e-103;
Matches 218; Conservative 0; Mismatches 0;
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99.1%; Pred. No. 2.3e-102;
tive 0; Mismatches 2;
                    PRIOR APPLICATION NUMBER: 09/809,746
PRIOR FILING DATE: 2001-03-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 222
2002-08-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 67.1
Best Local Similarity 99.1
Matches 216; Conservative
                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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  CURRENT FILING DATE:
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Patent No. 6889145
GENERAL INFORMATION:
APPLICANT: Jardetzky, Theodore S.
TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A FC REGION OF AN IGE ANTIBODY AND FILE REFERENCE: AL-9-C3
FILE REFERENCE: AL-9-C3
CURRENT APPLICATION NUMBER: US/10/211,948
                                                             Sequence 1, Application US/09701623C

Sequence 1, Application US/09701623C

Sequence 1, Application US/09701623C

GENERAL INFORMATION:

APPLICANT: Wang Ph.D., Chang Yi

TITLE OF INVENTION: ALLERGY

TITLE OF INVENTION: ALLERGY

FILE REFERENCE: 115441530G1

CURRENT PELING DATE: 12000-12-01

PRIOR APPLICATION NUMBER: DCT/US99/13959

PRIOR APPLICATION NUMBER: 097/00,287

PRIOR APPLICATION NUMBER: 091/10,287

PRIOR FILING DATE: 1998-06-20

NUMBER OF SEQ ID NOS: 91

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1

LENGTH: 325

TANDER DATE: 1938-06-20

SEQ ID NO 1

LENGTH: 325
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Pred. No. 1.2e-155;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: CH2CH3 of human IGE PUBLICATION INFORMATION:
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Best Local Similarity 99.4%;
Matches 318; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS: Dorrington,
AUTHORS: Bennich,
JOURNAL: Immunology
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ORGANISM: HUMAN
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; DATE: 1978
US-09-701-623C-1
                          RESULT 2
US-09-701-623C-1
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RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAF-ATPEWPGSRDKRTLACLI 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 PPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMD--VDLSTASTTQE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 PPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTWLVDGQBAENLFPYTTRPKREG 81
                                                                                                                                                                                                                                                                                                                                                                                                                                               60.8%; Score 1038.5; DB 2; Length 342; 62.4%; Pred. No. 9.9e-92; Live 41; Mismatches 73; Indels 7;
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APPLICANT: HOLLIS, GREGORY F.
APPLICANT: PATEL, MAYUR D.
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Synthetically generated proteins
                                                                    TITLE OF INVENTION: ENHANCED VACCINES FILE REFERENCE: 10223/06601
CURRENT APPLICATION NUMBER: US/09/401,636
CURRENT FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FASELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                  SEQ ID NOS: 11
FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 RAVHEAASPSQTVQRAVSVNPG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               320 RVVHEALPGSRTLEKSLHYSAG 341
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5629415
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126 E. LINCOLN AVENUE
               Sequence 8, Application US/09401636
Patent No. 6913749
                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 62.4%
Matches 201; Conservative
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STATE: NEW JERSEY
COUNTRY: USA
                                                           GENERAL INFORMATION:
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.09-401-636-8
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EGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPF 119
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GENERAL INFORMATION:
APPLICANT: HOLLIS, GREGORY F.
APPLICANT: PATEL, MAYUR D.
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 4
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13795
                                                                                                                                                                                                                                                                                                                                                                                             56.0%; Score 956.5; DB 1;
56.2%; Pred. No. 1.1e-83;
iive 50; Mismatches 87;
     Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: CHRISTINE E. CARTY
126 E. LINCOLN AVENUE; P.O. BOX 2000
SOFTWARE: Patentin No. CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,583
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFENCE/DOCKET NUMBER: 19211
TELECOMMUNICATION: TELEPHONE: (908) 594-6734
TELEPHONE: (908) 594-4720
INPORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids

"WITH ALSO AMINO ACID
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Best Local Similarity 56.2%
Matches 182; Conservative
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ADDRESSEE: CHRISTINE
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ZIP: 07065-0907
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FILING DATE

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; Sequence 11, Application US/09479614
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
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                                                                                                                                                                                                                           Length 426;
                                                                                                                                                                                                                                                    50; Mismatches 87; Indels
                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                         56.0%; Score 956.5; DB 4 56.2%; Pred. No. 1.1e-83;
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CURRENT FILING DATE: 2000-01-07
EARLIER PILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 431
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ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19211Y
TELECOMMUNICATION INFORMATION:
TELEPRONE (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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Best Local Similarity 56.2%
Matches 182; Conservative
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Best Local Similarity 56.5
Matches 183; Conservative
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MOLECULE TYPE: protein
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ORGANISM: Felis catus
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PCT-US95-13795-2
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US-09-479-614-14
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US-09-479-614-14
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Sequence 2, Application US/09479614

Patent No. 6573372

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: McCall, Catherine

APPLICANT: Weber, Eric

TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods

TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods

TITLE APPLICANT: Wober, Exic

CURRENT APPLICATION UNMBER: US/09/479,614

CURRENT APPLICATION NUMBER: 60/115,033

EARLIER PILING DATE: 1999-01-07

SEALIER PILING DATE: 1999-01-07

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NOS: 34

SEQ ID NO 2.
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FIPPTVKLFHSSCNPLGDTGSTIQLLCLISGYVPGDMEVTWLVDGQKATNIFPYTAPGKQ 168
                                              EGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPF 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
55.6%; Score 949.5; DB 2
Best Local Similarity 56.5%; Pred. No. 6.5e-83;
Matches 183; Conservative 46; Mismatches 90
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ORGANISM: Felis catus
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| Sequence 2, Application US/09701623C
| Patent No. 6811782
| GENERAL INFORMATION:
| APPLICANT: Wang Ph.D., Chang Yi
| TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
| TITLE OF INVENTION: ALLERGY
| TITLE OF INVENTION: ALLERGY
| FILE REFERENCE: 11514153US1
| CURRENT PILING DATE: 2000-12-01
| PRIOR APPLICATION NUMBER: 09/100,287
| PRIOR PILING DATE: 1999-06-20
| PRIOR PILING DATE: 1998-06-20
| PRIOR FILING DATE: 1998-06-20
| NUMBER OF SEQ ID NOS: 91
| SEQ ID NO 2
| LENGTH: 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEBKQRNGTLTVTSTLPVG 179
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                                             APPLICANT: McCall, Catherine
APPLICANT: McCall, Catherine
APPLICANT: Weber, Eric
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
FILE REFERENCE: P-1047
CURRENT APPLICATION NUMBER: US/09/479,614
CURRENT FILING DATE: 2000-01-07
EARLIER APPLICATION NUMBER: 60/115,033
EARLIER FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                           1 PTPPTVKILQSSCDGGGHPPPTIQLLCLVSGYTPGTINITWLEDGQ-VMDVDLSTASTTQ
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56.5%; Pred. No. 6.5e-83;
ive 46; Mismatches 90;
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US-09-479-614-29
; Sequence 29, Application US/09479614
; Patent No. 6573372
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Best Local Similarity 56.5
Matches 183; Conservative
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; ORGANISM: Felis catus
US-09-479-614-29
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ORGANISM: Dog
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OTHER INFORMATION: CH2CH3n of dog IgE

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                                                                                                                                                                                                                                                1 PTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQ-VMDVDLSTASTTQ
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                                                                                                                                                                  Length 312;
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                                                                                                                                                                                                            Indels
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                                                                                                                                                                Query Match 52.5%; Score 895.5; DB 2; Best Local Similarity 55.1%; Pred. No. 5.3e-78; Matches 172; Conservative 48; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 49.7%; Pred. No. 2.4e-71;
Matches 160; Conservative 58; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/09401636
; Sequence 11, Application US/09401636
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION WUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
LENGIH: 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COVVHEALSGSR 312
                    AUTHORS: Patel,
JOURNAL: Immunogenetics
VOLUME: 41
PAGES: 282-286
PUBLICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 LYVHKAPKITCLVVDLATMEG-MNLTWYRESKEPVNPGPLNKKDHFNGTITVTSTLPVNT 200
                          181 RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAF-ATPEWPGSRDKRTLACLI 239
                                                                              ONFMPEDISVOWLHNEVOLPDARHSTTOPRKTKGS--GFFVFSRLEVTRAEWEOKDEFIC 297
                                         NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSG--FFVFSRLEVTRAEWEQKDEFICR
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47.4%; Pred. No. 4.6e-68;
tive 54; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Synthetically generated proteins
                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Hellman, Lars T.
TITLE OF INVENTION:
FILE REFERENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/09/401,636
CURRENT APPLICATION NUMBER: US/09/401,636
CURRENT FILING DATE: 1999-09-22
PRIOR PILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 340
                                                                                                                                 RAVHEAASPSQTVQRAVSVNPG 319
                                                                                                                                                         319 RVVHEALPGSRTLEKSLHYSAG 340
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Patent No. 6913749
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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61 GELASTOSELTLSOKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT 180
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49.2%; Pred. No. 3.8e-67;
iive 49; Mismatches 100; Indels
FILLE OF INVENTION: ALLERGY
CURRENT APPLICATION NUMBER: US/09/701,623C
CURRENT APPLICATION NUMBER: US/09/701,623C
FILOR APPLICATION NUMBER: PCT/US99/13959
FRIOR APPLICATION NUMBER: PCT/US99/13959
FRIOR FILING DATE: 1999-06-21
FRIOR FILING DATE: 1998-06-20
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PATENTIN VEY: 2.1
SOFTWARE: PATENTIN VEY: 2.1
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OTHER INFORMATION: CH2CH3 of
PUBLICATION INFORMATION:
AUTHORS: Dorrington,
AUTHORS: Bennich,
JOURNAL: Immunology
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Best Local Similarity 49.24
Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS: Patel,
JOURNAL: Immunogenetics
VOLUME: 41
PAGES: 282-286
DATE: 1995
PUBLICATION INFORMATION:
AUTHORS: Steen,
VOLUME: 177
VOLUME: 177
PAGES: 19-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAGES: 3-25
DATE: 1978
PUBLICATION INFORMATION:
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PUBLICATION INFORMATION:
AUTHORS: Ishida,
JOURNAL: EMBO J.
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DATE: 1982
                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: RAT
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RESULT 15

Sequence 3, Application US/09701623C
Patent No. 6811782
GENERAL INFORMATION
APPLICANT: WANG Ph.D., Chang Yi
TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF

US-09-701-623C-3

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                                                                                                                                                                                                                                                                                                                                                                                                       8; Gaps
                                                                                                                                                                                                                                                                                                                                           Query Match 45.8%; Score 781; DB 2; Length 341; Best Local Similarity 47.8%; Pred. No. 6.6e-67; Matches 154; Conservative 59; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-3
; Sequence 3, Application US/09401636
; Patent No. 613749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOG ID NO 3
; ERWITH 341
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                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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Search completed: November 30, 2005, 01:12:52 Job time : 39.2609 secs

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; ORGANISM: Homo sapiens
US-09-847-208-6
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Sequence 1, Appli
Sequence 97, Appl
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 1, Appli
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Sequence 1, Appli
Sequence 60, Appl
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 45, Appli
Sequence 37, Appli
Sequence 37, Appli
Sequence 176, Appl
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1, Appli
1, Appli
                                                               November 30, 2005, 00:56:45; Search time 133.913 Seconds (without alignments) 998.449 Million cell updates/sec
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| cgn2_6/ptodata/1/pubpaa/USO*_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO*_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO*_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO*_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USIA_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USII_FUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USII_FUBCOMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
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US-00-439-6

US-09-949-375A-2

US-09-949-375A-6

US-09-949-375A-6

US-10-363-954A-2

US-10-363-954A-2

US-10-363-954A-6

US-10-10-664-1

US-10-10-664-1

US-10-10-655-329

US-10-627-556-174

US-10-627-556-174

US-10-627-556-174

US-09-947-208-5

US-00-947-208-5

US-09-947-208-5

US-09-947-208-5

US-09-947-208-5

US-09-947-208-5

US-09-947-208-5

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US-09-947-208-5

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US-10-000-439-7
US-10-047-542-45
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Maximum Match 100%
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Perfect score:
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Sequence 384, App
Sequence 134, App
Sequence 129, App
Sequence 176, App
Sequence 180, App
Sequence 180, App
Sequence 8, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 34, Appli
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US-10-363-954A-8
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US-10-910-811-34
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ALIGNMENTS

NEESULT 1 US-09-817-208-6 SQUENCE 6, Application US/09847208 Publication No. US2030082190A1 GENERAL INFORMATION: APPLICANT: Shang, Ke APPLICANT: Zhang, Ke TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES CURRENT FILING DATE: 2001-05-01 NUMBER OF SEQ ID NOS: 177 SOFTWARE: FASESEQ for Windows Version 4.0 SEQ ID NO 6	; LENGTH: 320 ; TYPE: PRT	OND THE COUNTY OF THE COUNTY O
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	Gaps	ASTTOE
320;	0 ;	DVDLST
Length	Indels	YLEDGQVM
DB 3;		PGTINITA
100.0%; Score 1707; DB 3; Length 320;	, Mismatches	1 FTPPTVKILOSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE 60
	ative 0	SSCDGGGHFP
Query Match	Dest notal samilarity 100.0%; from No. 2.10.2%; Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps	OV 1 FTPPTVKILO

	301 HEAASPSQTVQRAVSVNPGK 320	301	ò
300	NEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV	241	qq
300	NEMPEDI SVQMLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEMEQKDEFICRAV	241	δλ
240	181 RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ	181	qq
240	RDWIEGETYQCRUTHPHLPRALMRSTTKTSGPRAAPEUYAFATPEWPGSRDKRTLACLIO	181	δ
180	LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT	121	QQ
180	121 LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT	121	ò
120	61 GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD	61	q
120	61 GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD	61	ò
09	FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE	7	q
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OTHER INFORMATION: Human IgE heavy chain C3 domain
                                                                                         FEATURE:
NAME/KEY: MISC_FEATURE
                                                                                                                                                                                    NAME/KEY: MISC FEATURE LOCATION: (212)..(215)
                                                                                                                                                                                                                                                                  NAME/KEY: MISC FEATURE LOCATION: (100)..(114)
                                                                                                                                                                                                                                                                                                                                           NAME/KEY: MISC FEATURE LOCATION: (210)..(218)
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       US-10-00-439-6

Sequence 6, Application US/10000439

Publication No. US20030064063A1

GENERALI INFORMATION:

APPLICANT: Saxon, Andrew

TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR

TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES

FILE REPRENCE: UCO67.004A

CURRENT FILING DATE: 2001-02-4

PRIOR PRIOR FILING DATE: 2001-05-01

NUMBER OF SEQ ID NOS: 13

SOFTWARRE: FastSEQ for Windows Version 4.0

LENGTH: 320
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Sequence 2, Application US/09949375A
Sequence 2, Application US/09949375A
Setence No. US20020172673A1
GENERAL INFORMATION:
APPLICANT: KLISENER, Steen et al.
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
FILE REFERENCE: 3631-0111P
CURRENT APPLICATION NUMBER: US/09/949,375A
CURRENT FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 1707; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.4e-127;
Matches 320; Conservative 0; Mismatches 0;
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LOCATION: (8)..(103)
OTHER INFORMATION: Human 1gE heavy chain C2 domain
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                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: homo sapiens
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NAME/KEY: DOMAIN
LOCATION: (112)..(211)
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US-09-949-375A-2
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US-09-949-375A-4
; Sequence 4, Application US/09949375A
; Patent No. US20020172673A1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen et al.
; FILLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
; FILL REPERENCE: 3631-0111P
; CURRENT APPLICATION NUMBER: US/09/949,375A
                                                                                                                                                                                                                                                                                                and
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                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (1007..(114)
OTHER INFORMATION: Epitope including C2C3 linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (210)..(218)
OTHER INFORMATION: Epitope including C3C4 linker
                                                                                                                                                LOCATION: (104)..(111)
OTHER INFORMATION: Linker between domains C2
                                                                                                                                                                                                                                                                                                ប
NAME/KEY: DOMAIN
LOCATION: (216)..(317)
OTHER INFORMATION: Human IGE heavy chain C4
                                                                                                                                                                                                                                                                       LOCATION: (212)..(215)
OTHER INFORMATION: Linker between domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (139)...(145)
OTHER INFORMATION: Epitope in BC loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MISC FEATURE
LOCATION: (167)...(175)
OTHER INFORMATION: Epitope in DE loop
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: MISC FEATURE
LOCATION: (196)...(206)
OTHER INFORMATION: Epitope in FG loop
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PRIOR APPLICATION DATE: 2003-03-06; PRIOR APPLICATION NUMBER: US 60/232,831
; PRIOR FILING DATE: 2000-09-15; PRIOR FILING DATE: 2000-09-06; NUMBER OF SEQ ID NOS: 38; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2; LENGTH: 323; TENGTH: 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (216)..(317)
OTHER INFORMATION: Human IGE heavy chain C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (8)..(103)
OTHER INFORMATION: Human 19E heavy chain C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: DOMAIN
LOCATION: (112)..(211)
OTHER INFORMATION: Human 19B heavy chain
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OTHER INFORMATION: Epitope in DE loop
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OTHER INFORMATION: Epitope
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NAME/KEY: MISC FEATURE
TATALON: (212)..(215)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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                                                                                                                                    , OTHER INFORMATION: Artificial amino acid sequence of SEQ ID NO: US-09-949-375A-4
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Best Local Similarity 100.0%; Pred. No. 2.4e-127;
Matches 320; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                         Length 323;
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Batent No. US20020172673A1

GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION METHOD FOR DOWN-REGULATING IGE
FILE REFERENCE: 3631-0111P
CURRENT APPLICATION NUMBER: US/09/949,375A

CURRENT PILING DATE: 2002-01-18

NUMBER OF SEQ ID NOS: 38

SOFTWARE: PatentIn version 3.1

SEQ ID NO 6

LENGTH: 323
                                                                                                                                                                                         100.0%; Score 1707; DB 3;
100.0%; Pred. No. 2.4e-127;
tive 0; Mismatches 0;
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ORGANISM: Artificial Sequence
                NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
                                                                                       TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                             Conservative
 CURRENT FILING DATE:
                                                                                                                                                                                                             Similarity
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US-09-949-375A-6
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Sequence 2, Application US/10363954A
Sublication No. US20040156838A1
GENERAL INFORMATION:
APPLICANT: KLYSNER, Steen et al.
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
FILE REFERENCE: 4614-0115P
CURRENT APPLICATION NUMBER: US/10/363,954A
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OTHER INFORMATION: Linker between domains C3 and
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OTHER INFORMATION: Linker between domains C2 and
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LOCATION: (210)..(218)
OTHER INFORMATION: Epitope including C3C4 linker
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OTHER INFORMATION: Epitope including C2C3 linker
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GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD 123
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Publication No. US20040156838A1

GENERAL INFORMATION:
    GENERAL INFORMATION:
    TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
    TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
    CURRENT APPLICATION NUMBER: US/10/363,954A
    CURRENT FILING DATE: 2003-03-06
    PRIOR PELLIGN NUMBER: US 60/232,831
    PRIOR FILING DATE: 2000-09-15
    PRIOR FILING DATE: 2000-09-16
    NUMBER OF SEQ ID NOS: 38
    NUMBER OF SEQ ID NOS: 38
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100.0%; Pred. No. 2.4e-127;
iive 0; Mismatches 0;
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Matches 320; Conservative
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US-10-363-954A-6
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                                                                                                           Length 323;
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Publication No. US20040156838A1
GENERAL INFORMATION:
APPLICANT: KIYSNER, Steen et al.
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
FILE REFERENCE: 4614-0115P
CURRENT APPLICATION NUMBER: US/10/363,954A
CURRENT FILING DATE: 2003-03-06
PRIOR APPLICATION NUMBER: US 60/232,831
PRIOR PILING DATE: 2000-09-15
PRIOR PILING DATE: 2000-09-16
PRIOR PILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.1
                                                                                                       100.0%; Score 1707; DB 4;
100.0%; Pred. No. 2.4e-127;
iive 0; Mismatches 0;
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; OTHER INFORMATION: Human IGE heavy chain C1 domain US-10-363-954A-4
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                     LOCATION: (1967. (206)
COTHER INFORMATION: Epitope in FG loop
US-10-363-954A-2
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ORGANISM: Artificial Sequence
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Matches 320; Conservative
                                                                                                     Query Match
Best Local Similarity 100.
Matches 320; Conservative
      NAME/KEY: MISC FEATURE
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US-10-363-954A-4
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LENGTH: 323
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                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; ; OTHER INFORMATION: amino acid sequence
US-10-627-556-224
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100.0%; Pred. No. 2.5e-127;
tive 0; Mismatches 0;
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Patent No. US20010038843A1
GENERAL INFORMATION:
APPLICANT: Hellman, Lars T.
TITLE OP INVENTION: ENTRANCED VACCINES
PILE REFERENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/09/401,636
CURRENT FILING DATE: 1999-09-22
PRIOR FILING DATE: 1998-11-02
                                     Sequence 224, Application US/10627556 Publication No. US20050136049A1 GENERAL INFORMATION:
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Matches 320; Conserv
                             US-10-627-556-224
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100.0%; Score 1707; DB 4; Length 331;
Best Local Similarity 100.0%; Pred. No. 2.5e-127;
Matches 320; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                        Length 331;
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                                                                                                                                           ; OTHER INFORMATION: Synthetically generated proteins US-09-401-636-1
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100.0%; Score 1707; DB 3;
Best Local Similarity 100.0%; Pred. No. 2.5e-127;
Matches 320; Conservative 0; Mismatches 0;
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; Publication No. US20030031663A1
; GENERAL INFORMATION:
    APPLICANT: Hellman, Lars T.
    TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-22
; PRIOR FILING DATE: 1999-11.02
; PRIOR FILING DATE: 1999-11.03
; SROFTWARE: PRESEQ for Windows Version 4.0
; SEQ ID NO 1.
SEQ ID NOS: 11
FastSEQ for Windows Version 4.0
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                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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                                   LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT 180
                                                         RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 251
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Publication No. US20030118592A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069-401C1
CURRENT APPLICATION NUMBER: US/10/207,655
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
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100.0%; Pred. No. 2.5e-127;
tive 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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Matches 320; Conservative
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US-10-207-655-329
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US-10-673-594-1
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Sequence 1, Application US/10673594 Publication No. US20040076625A1

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61 GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTPEDSTKKCADSNPRGVSAYLSRPSPFD 120
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Sequence 97, Application US/10627556
Publication No. US20050136049A1
GENERAL INFORMATION:
APPLICANT: LEDBETTER, JEFFREY A.
APPLICANT: HAYDEN-LEDBETTER, MARTHA
APPLICANT: THOMPSON, PETER A.
TILLE OF INVENTION: BINDING CONSTRUCTS AND METHODS FOR USE THEREOF
FILE REFERENCE: 49076.000004.CTP2
CURRENT APPLICATION NUMBER: US/10/627,556
CURRENT FILING DATE: 2003-07-26
PRIOR PELICATION NUMBER: 10/053,530
PRIOR PELLING DATE: 2002-01-17
PRIOR PELLING DATE: 2002-01-17
PRIOR APPLICATION NUMBER: 09/765,208
PRIOR PELLING DATE: 2002-01-17
PRIOR APPLICATION NUMBER: 09/765,208
PRIOR PELLING DATE: 2002-01-07
PRIOR FILING DATE: 2002-01-07
PRIOR PELLING DATE: 2002-01-07
PELLING DATE: 2002-
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US-10-673-594-1
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100.0%; Pred. No. 2.5e-127;
iive 0; Mismatches 0;
TITLE OF INVENTION: ENHANCED VACCINES
FILE REPERENCE: 1022/3/006001
CURRENT APPLICATION NUMBER: US/10/673,594
CURRENT FILING DATE: 2003-09-29
PRIOR APPLICATION NUMBER: US/09/401,636
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO I
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 320; Conservative
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PUBlication No. US20050136049A1

GENERAL INFORMATION:

APPLICANT: LEDBETTER, JEFFREY A.

APPLICANT: THOMESON, PETER A.

TITLE OF INVENTION: BINDING CONSTRUCTS AND METHODS FOR USE THEREOF

FILE REFERENCE: 49076.000004.CIP2

CURRENT APPLICATION NUMBER: US/10/627,556

CURRENT PILING DATE: 2003-07-26

PRIOR FILING DATE: 2002-01.17

PRIOR FILING DATE: 2002-01.16

PRIOR FILING DATE: 2002-01.16

PRIOR FILING DATE: 2001-01.16

PRIOR FILING DATE: 2001-01.17

PRIOR FILING DATE: 2001-01.17
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100.0%; Score 1707; DB 5;
Best Local Similarity 100.0%; Pred. No. 2.5e-127;
Matches 320; Conservative 0; Mismatches 0;
                                                                                                                 100.0%; Score 1707; DB 5;
llarity 100.0%; Pred. No. 2.5e-127;
Conservative 0; Mismatches 0;
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US-10-627-556-174
        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-627-556-97
                                                                                                                                                     Similarity
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US-10-627-556-174
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Best Local Simi
Matches 320;
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181 RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
                                                                                            241 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV 300
                                                                                                                                                                                    248 NFMPEDISVQMLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV 307
Search completed: November 30, 2005, 01:16:49 Job time : 134.913 secs
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121 LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEBKQRNGTLTVTSTLPVGT 180
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ORGANISM: HUMAN
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1 FTPPTVKILQSSCDGGGHFP......HEAASPSQTVQRAVSVNPGK 320
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1: /cgn2_6/ptodata/2/pubpaa/US10 NEW PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US07 NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US08 NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US17 NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
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US-10-723-207-4
US-11-144-248-45
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US-11-144-248-50
US-11-025-712-12
US-11-025-289-6
US-11-022-289-7
US-11-022-289-7
US-11-022-289-3
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Maximum Match 100%
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Perfect score:
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Maximum DB
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GENERAL INFORMATION: US2005025034A1

SEQUENCE 1, Application US/10723207

Publication No. US2005025034A1

GENERAL INFORMATION:

APPLICANT: Wang, Chang Yi

APPLICANT: Walfield, Alan M.

TITLE OF INVENTION: BEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF

TITLE OF INVENTION: ALLERGY

TITLE OF INVENTION: ALLERGY

FILE REFERENCE: 1151-4153U32

CURRENT APPLICATION NUMBER: US/10/723,207

CURRENT APPLICATION NUMBER: US/10/723,207

CURRENT APPLICATION NUMBER: O9/701,623

PRIOR PILING DATE: 2000-12-01

PRIOR FILING DATE: 1999-06-21

PRIOR FILING DATE: 1999-06-21

PRIOR FILING DATE: 1999-06-21

PRIOR FILING DATE: 1999-06-21

PRIOR FILING DATE: 1999-06-20

NUMBER OF SEQ ID NOS: 91

SOFTWARE: PATENTIN VOY: 2.1

SEC ID NOS: 91

SEC ID NOS: 91
Sequence 6, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 16, Appl
Sequence 12, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 19, Appl
Sequence 19, Appli
Sequence 18, Appli
Sequence 18, Appli
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Sequence 18, Appli
Sequence 39, Appli
Sequence 30, Appli
Sequence 2, Appli
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al Similarity 99.6%; Score 1701; DB 1; 1
al Similarity 99.4%; Pred. No. 1.4e-111;
318; Conservative 2; Mismatches 0;
  US-11-016-503-6

US-11-016-503-4

US-11-016-503-1

US-11-016-503-15

US-11-016-503-16

US-11-016-503-17

US-11-016-503-17

US-11-016-503-17

US-10-949-720-390

US-10-949-720-389

US-11-008-727-14

US-11-008-727-14

US-11-008-727-14

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US-11-008-727-20
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OTHER INFORMATION: CH2CH3 of human IGE
PUBLICATION INFORMATION:
        AUTHORS: Dorrington,
AUTHORS: Bennich,
JOURNAL: Immunology
VOLUME: 41
PAGES: 3-25
JOATE: 1978
US-10-723-207-1
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; Publication No. US20050250934A1
; Bublication No. US20050250934A1
; GENERAL INFORMATION:
; Publication No. US20050250934A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; APPLICANT: Walfield, Alan M.
; TITLE OF INVENTION: ALLERGY
; TITLE OF INVENTION: ALLERGY
; FILE REFERENCE: 1151-4153U62
; CURRENT APPLICATION NUMBER: US/10/723,207
; CURRENT APPLICATION NUMBER: US/10/10,623
; PRIOR APPLICATION NUMBER: 09/701,623
; PRIOR FILING DATE: 1999-06-21
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PATENTIN VOIC: 2.1
; SEQ ID NO 3
; LIENGTH: 313
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45.9%; Score 783; DB 1; Length 313;
Best Local Similarity 49.2%; Pred. No. 3.1e-48;
Matches 150; Conservative 49; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
OTHER INFORMATION: CH2CH3 of rat IgE
OTHER INFORMATION:
AUTHORS: Dorrington,
AUTHORS: Bennich,
JOHRNAL: Immunology
VOLUME: 41
                      297 CRAVHEAASPSQ 308
                                                                301 COVVHEALSGSR 312
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JOURNAL: J. Mol. Biol.
VOLUME: 177
PAGES: 19-32
DATE: 1984
AUTHORS: Ishida,
JOURNAL: EMBO J.
VOLUME: 1
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JOURNAL: Immunogenetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAGES: 282-286
DATE: 1995
PUBLICATION INFORMATION:
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DATE: 1978
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APPLICANT: Walfield, Alan M.
TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
TITLE OF INVENTION: ALLERGY
FILE REFERENCE: 1151-4153US2
CURRENT APPLICATION NUMBER: 09/701,623
PRIOR PILING DATE: 2000-12-01
PRIOR PLING DATE: 2000-12-01
PRIOR PLING DATE: 1999-06-21
PRIOR PILING DATE: 1999-06-20
NUMBER OF SEQ ID NOS: 91
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RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
                                                                                         NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV 300
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                                                                                                                                                                                                                                                301 HEAASPSQTVQRAVSVNPGK 320
                                                                                                                                                                                                                                                                                         HEAASPSQTVQRAVSVNPGK 325
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Matches 172; Conservative
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JOURNAL: Immunogenetics
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DATE: 1995
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ORGANISM: Dog
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LENGTH: 312
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Publication No. US20050250934A1

GENERAL INFORMATION:

APPLICANT: Wang, Chang Yi

APPLICANT: Wang, Chang Yi

TITLE OF INVENTION: ALLERGY

TITLE OF INVENTION: ALLERGY

TITLE OF INVENTION: ALLERGY

TITLE OF INVENTION: ALLERGY

CURRENT APPLICATION NUMBER: US/10/723,207

CURRENT PILING DATE: 2003-11-24

PRIOR FILING DATE: 2000-12-01

PRIOR PILING DATE: 1999-06-21

PRIOR PILING DATE: 1998-06-21

PRIOR APPLICATION NUMBER: 09/100,287

PRIOR APPLICATION NUMBER: 09/100,287

NUMBER OF SEQ ID NOS: 91

SEQ ID NO 4

LENGTH. 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 LVVDLAPSKGTVNITWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGTRDWIEGETYQC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192 RVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQNFMPEDISVQW 251
                                 RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
                                                   241 NEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSG--FFVFSRLEVTRAEWEQKDEFICR 298
                                                                                                                  244 NFFPEDISVQWLQDSKLIPKSQHSTTTPLKTNGSNQRFFIFSRLEVTKALWTQTKQFTCR 303
126 LYENGTPKLITCLVLDL-ESEENITVTWVRERKKSIGSASQRSIKHHNATISIISILPVDA 184
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                                                                                                                                                                     299 AVHEA 303
                                                                                                                                                                                                   304 VIHEA 308
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ORGANISM: MOUSE
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US-11-144-248-45
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Sequence 45, Application US/11144248 Publication No. US20050244408A1 GENERAL INFORMATION:

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APPLICANT: Cohen, Bruce D.
APPLICANT: Gohen, Bruce D.
APPLICANT: Beebe, Jean
APPLICANT: Miller, Penelope E.
APPLICANT: Miller, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Gorvalan, Jose R.
APPLICANT: Gallo, Michael B.
TILE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR TILE REFRENCE: ABX-PF2
CURRENT APPLICATION NUMBER: US/11/144,248
CURRENT FILING DATE: 2005-06-02
PRIOR PILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 06/259,927
PRIOR PILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 46
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                                                                 APPLICANT: COTVAIN, JOSE R.
APPLICANT: COTVAIN, JOSE R.
APPLICANT: CATVAIN, JOSE R.
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTHBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR FILE REFERENCE: ABX-PP2
CURRENT APPLICATION NUMBER: US/11/144,248
CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US/10/038,591
PRIOR FILING DATE: 2002-01-04
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 45
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31.3%; Pred. No. 2.3e-23;
ive 60; Mismatches 139;
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Beebe, Jean
Miller, Penelope
Moyer, James D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-45
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Best Local Similarity
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APPLICANT: Beebe, Jean
APPLICANT: Miller, Penelope E.
APPLICANT: Miller, Penelope E.
APPLICANT: Miller, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Corvalan, Jose R.
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR FILE REPRENCE: ARX-PF2
CURRENT APPLICATION NUMBER: US/11/144,248
CURRENT FILING DATE: 2002-06-02
PRIOR PILING DATE: 2002-01-04
PRIOR FILING DATE: 2002-01-04
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.1
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--RGVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEE 163
                                                                                                                                                            224 PEWPGSRDKRT----LLACLIQNEMPEDISVOWLHNEVQLPDARHSTTQPRKTKGSGFFV 278
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                       KQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFAT
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Best Local Similarity 31.3
Matches 107; Conservative
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ORGANISM: Homo sapiens
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LENGTH: 473
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APPLICANT: Cohen, Bruce D.

APPLICANT: Beebe, Jean

APPLICANT: Beebe, Jean

APPLICANT: Mailer, Penelope E.

APPLICANT: Moyer, James D.

APPLICANT: Gallo, Michael

TITLE OF INVENTION: MICHAEl

TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR

FILE REFERENCE: ABX-PF2

CURRENT FILING DATE: 2005-06-02

PRIOR FILING DATE: 2005-06-02

PRIOR FILING DATE: 2002-01-04

PRIOR FILING DATE: 2002-01-04

PRIOR FILING DATE: 2001-01-05

NUMBER OF SEQ ID NOS: 60

SOFTWARE: Patentin Ver. 2.1

SEQ ID NOS: 60

SEQ ID NOS: 60

SEQ ID NOS: 60

SEQ ID NOS: 60
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                                                                                                            Length 470;
                                                                                                       ; Score 425; DB 7; Length 47; Pred. No. 2.3e-23; 60; Mismatches 139; Indels
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                                                                                                                                                  Matches 107; Conservative
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ORGANISM: Homo sapiens
US-11-144-248-49
      ; LENCTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-46
                                                                                                       Query Match
Best Local Similarity
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PSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTS 174
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Sequence 28, Application US/11144248
Publication No. US20050244408A1
GENERAL INFORMATION:
APPLICANT: Cohen, Bruce D.
APPLICANT: Beebe, Jean
APPLICANT: Moyer, James D.
APPLICANT: Gorvalan, Jose R.
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR FILE REFERENCE: ABX-PP2
CURRENT APPLICATION NUMBER: US/11/144,248
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TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
TITLE REFERENCE: 185831/US/2
CURRENT APPLICATION NUMBER: US/11/022,289
CURRENT FILING DATE: 2004-12-21
PRIOR APPLICATION NUMBER: US 60/531,752
PRIOR APPLICATION NUMBER: US 60/531,752
PRIOR FILING DATE: 2003-12-22
SOFTWARE: PALENCE: 15
SOFTWARE: PALENCE: PALENCE: 15
SOFTWARE: PALENCE: PALENCE: 
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Best Local Similarity 30.2%; Pred. No. 7.2e-23;
Matches 100; Conservative 57; Mismatches 136;
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                                                                                                                                                                                                                                                                                                                                   ; Sequence 6, Application US/11022289; Publication No. US20050249723A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 -RGVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORNGTLIVISTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTIKTSGPRAAPEVYAFAIP 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225 EWPGSRDKRT----LACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVF 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 VKILOSSCDGGGHFP-----PTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 STIQEGELASTQSELTLSQKHWLSDRTYTCQVTYQ-GHTFEDST---KKCADSNP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                       Sequence 12, Application US/11025712
Publication No. US20050255108A1
GENERAL INFORMATION:
APPLICANT: Bednar, Martin M.
Thomas, G. Roger
Gross, Cordell E.
TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
STREET: 1 DNA WAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1EM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/025,712
FILING DATE: 28-Dec-2004
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.7%; Score 422; DB 7; 31.1%; Pred. No. 3.6e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/10/404,286
FILING DATE: 31-Mar-2003
APPLICATION NUMBER: 09/811384
FILING DATE: 20-DEC-2000
APPLICATION NUMBER: 09/251652
FILING DATE: 17-FEB-2000
APPLICATION NUMBER: 06/78800
FILING DATE: 22-JAN-1997
APPLICATION NUMBER: 60/093038
APPLICATION NUMBER: 60/093038
APPLICATION NUMBER: 23-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Evans, David W.
REGISTRATION NUMBER: NONE
FEFERENCE/DOCKET NUMBER: P1729C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 450 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650/952-9881.
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 31.13
Matches 106; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-11-025-712-12
                                                   US-11-025-712-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        354 TLMISRIPEVTCVVVDVSHEDDEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            354 TLMISRIPEUTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL 413
                                                                                                                                                                                                                                                                              294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235 LACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDE 294
:: | :: | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | | :: | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: 
                                                                                                     121 -LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 TRDWIEGETYOCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRT----
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                                                                                                                                                                                                                                                                                                                                                                         235 LACLIQNEMPEDISVONLHNEVOLPDARHSTTOPRKTKGSGFFVFSRLEVTRAEWEQKDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: LATERATION:
APPLICANT: LAGARY, Gregory Alan
TITLE OF INVENTION: FC POLYBEPTIDES WITH NOVEL FC LIGAND BINDING SITES
FILE REPERENCE: 186831/US/2
CURRENT APPLICATION NUMBER: US/11/022,289
PRIOR PAPLICATION NUMBER: US 60/531,752
PRIOR PAPLING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 15
SSEQ ID NO 8
LENGTH: 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 24.4%; Score 416; DB 7; Length 55
Best Local Similarity 30.1%; Pred. No. 1.1e-22;
Matches 98; Conservative 58; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295 FICRAVHEAASPSQTVQRAVSVNPGK 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | | :|||
FSCSVMHEALHNHYT-QKSLSLSPGK 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   295 FICRAVHEAASPSQTVQRAVSVNPGK 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | :|||
| S27 FSCSVMHEALHNHYT-QKSLSLSPGK 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/11022289; Publication No. US20050249723A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: Synthetic US-11-022-289-8
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US-11-022-289-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLT 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNP------RGVSAYLSRPSPFD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RDKRT-----LACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEV 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GELASTQSELTLSQKHWLSDRTYTCQVTYQ-GHTFEDST---KKCADSNP-----RGVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGLYSLSSVVTVPSSNF-GTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 AYLSRPSPFD-LPIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 LTVISTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 SSCDGGGHFP-----PTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
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TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
FILE REFERENCE: 186831/108/2
CURRENT APPLICATION NUMBER: US/11/022,289
CURRENT FILING DATE: 2004-12-21
PRIOR APPLICATION NUMBER: US 60/531,752
PRIOR FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.3
SEQ ID NO 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                24.4%; Score 416; DB 7; Length 326;
31.2%; Pred. No. 6.8e-23;
tive 59; Mismatches 136; Indels
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   CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US.10/038,591
PRIOR FILING DATE: 2002-01-04
PRIOR FILING DATE: 2001-04
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PATCHIN VET: 2.1
SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 7, Application US/11022289; Publication No. US20050249723A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ), OTHER INFORMATION: Synthetic US-11-022-289-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 31.2
Matches 105, Conservative
                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                    US-11-144-248-28
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Sequence 40, Application US/10723207

Publication No. US2005020934A1

GENERAL INFORMATION:

APPLICANT: Walfield, Alan M.

TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF TITLE OF INVENTION: US/10/723,207

CURRENT APPLICATION NUMBER: US/10/723,207

PRIOR FILING DATE: 1999-06-21

PRIOR APPLICATION NUMBER: PCT/US99/13959

PRIOR FILING DATE: 1999-06-21

PRIOR FILING DATE: 1999-06-20

NUMBER OF SEQ ID NOS: 91

SOFTWARE: PATENTIN VET. 2.1

SEQ ID NO 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    295 VDKSRWQQGNVFSCSVMHEA-LHNHYTQKSLSLSPGKPAPELLGGPSVFLFPPKPKDTLM 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 IRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGTRD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRT----LAC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 PPT-----IQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGELASTQSELT
                                                        APPLICANT: Lazar, Gregory Alan
TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
FILE REPREBLEGE: 185831/US/2
CURRENT APPLICATION NUMBER: US/11/022,289
CURRENT FILING DATE: 2004-12-21
PRIOR PAPLICATION NUMBER: US 60/531,752
PRIOR PILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.3
SEC ID NO 3
LENGTH: 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                         Length 548;
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24.3%; Score 414.5; DB 7; Length EBst Local Similarity 30.0%; Pred. No. 1.4e-22;
Matches 97; Conservative 59; Mismatches 136; Indels
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527 SVMHEALHNHYT-QKSLSLSPGK 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 RAVHEAASPSQTVQRAVSVNPGK 320
  Sequence 3, Application US/11022289 Publication No. US20050249723A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Synthetic US-11-022-289-3
                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial
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US-10-723-207-40
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                                                                                                                                                                                                                             Gaps
                                                                                                                                                           .;
0
OTHER INFORMATION: Description of Artificial Sequence: Peptide CHER INFORMATION: synthesized from amino acids with no genetic CHER INFORMATION: material as source US-10-723-207-40
                                                                                                         24.3%; Score 414; DB 1; Length 76;
100.0%; Pred. No. 2.2e-23;
:ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: November 30, 2005, 01:17:05 Job time : 7.37681 secs
                                                                                                                                                                                                                                                                                                 134 VDLAPSKGTVNLTWSR 149
                                                                                                                                                                                                                                                                                                                                           61 VDĽAPSKGTVNĽTWSR 76
                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 76; Conservative
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November 30, 2005, 00:33:18; Search time 10 Seconds (without alignments) 172.462 Million cell updates/sec
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3060
1 EPKSCDKTHICPPCPAPELL......HEAASPSQTVQRAVSVNPGK 569
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1: /cgn2 6/ptodata/2/pubpaa/US10 NEW PUB.pep:*

2: /cgn2 6/ptodata/2/pubpaa/US10 NEW PUB.pep:*

3: /cgn2 6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

4: /cgn2 6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

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6: /cgn2 6/ptodata/2/pubpaa/US01 NEW PUB.pep:*

7: /cgn2 6/ptodata/2/pubpaa/US11 NEW PUB.pep:*

8: /cgn2 6/ptodata/2/pubpaa/US11 NEW PUB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Appli Appli Appli Appli Appli Appli Appli Appl Appl Appli Appli Appli Appli 390, App Sequence 4, At Sequence 7, At Sequence 5, At Sequence 2, At Sequence 10, At Sequence 11, At Sequence 1, Description Sequence Seq Sequence 2 Sequence 3 Sequence 3 Sequence Sequence Sequence Sequence Sequence Sequence US-11-022-289-8 US-11-022-289-4 US-11-022-289-5 US-11-022-289-2 US-11-022-289-1 US-11-022-289-1 US-11-022-289-11 US-11-022-289-11 US-11-172-289-11 US-11-172-289-11 US-11-175-320-6 US-11-175-320-6 US-11-175-330-6 US-11-016-503-6 US-11-016-503-6 US-11-016-503-8 US-10-949-720-390 US-10-835-475-11 US-11-016-503-10 US-10-949-720-389 US-11-016-503-4 SUMMARIES % Query Match Length DB Score Result Š.

Sequence

Sequence 16, Appl Sequence 11, Appl Sequence 28, Appl Sequence 45, Appl Sequence 49, Appl Sequence 12, Appl Sequence 12, Appl Sequence 2, Appl Sequence 16, Appl Sequence 6, Appl Sequence 4, Appl Sequence 30, Appl Sequence 30, Appl Sequence 31, Appl Sequence 30, Appl
US-11-016-503-16 US-11-008-72-14 US-11-144-248-28 US-11-144-248-45 US-11-144-248-46 US-11-144-248-46 US-11-144-248-46 US-11-1025-712-12 US-10-025-712-12 US-10-025-712-12 US-10-008-727-40 US-11-008-727-40 US-11-008-727-40 US-11-008-727-40 US-10-008-727-40 US-10-723-207-41 US-10-723-207-31 US-11-0723-207-31 US-11-0723-207-31 US-11-0723-207-31 US-11-0723-207-31
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ALIGNMENTS

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Ö	FTPPTVKÍLÓSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE 6	GELASTOSELTLSOKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD 3	LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT 4
AS IMMUNOGEN FOR 7 7 1, DB 1; Lengtl 6.39-77; che 0, Inde: 8GYTPGTINITWLEDGG	SGYTPGTINITWLE	QGHTFEDSTKKCAD QGHTFEDSTKKCAD	ASGKPVNHSTRKEE
On US/10723207 150250934A1 1, Alan M. PEPTIDE COMPOSITION AS II ALLEGGY ALLEGGY ALLEGGY NUMBER: US/10/723,207 NUMBER: US/10/1,623 NUMBER: 09/701,623 NUMBER: 09/701,623 NUMBER: 09/100,287 1999-06-21 NUMBER: 09/100,287 1998-06-20 199	зсенгретіольсь	CHWLSDRTYTCQVTY	OLAPSKGTVNLTWSR
SULT 1 1-0-723-207-1 Sequence 1, Application US/10723207 Sequence 1, Application US/10723207 BublicanT: Wang, Chang Yi APPLICANT: Wang, Chang Yi APPLICANT: Wang, Chang Yi APPLICANT: Wang, Chang Yi TITLE OF INVENTION: ALLERGY FILE OF INVENTION: ALLERGY CURRENT FILING DATE: 2003-11-24 PRIOR PFLING DATE: 2000-12-01 PRIOR APPLICATION NUMBER: PCT/US99 PRIOR FILING DATE: 1998-06-21 PRIOR FILING DATE: 1998-06-20 SOFTWARE: PATON NUMBER: 09/100,2 TYPE: PRT ORGANISM: HUMAN FEATURE: CHANGES: BATORNICH, JOURNAL: Immunology VOLUME: 41 PAGES: 3-25 DATE: 1978 SECORGANISM: CADESTARING PRIOR SECONDICH, JOURNAL: Immunology VOLUME: 1978 SECORGALING PRIOR SECOMBENTING PRIOR SECONDICH, JOURNAL: IMMUNOLOGY VOLUME: 1978 SECORGALING PRIOR SECONDICH JOURNAL: IMMUNOLOGY VOLUME: 1978 SECORGALING PRIOR PRI	Freivkilóssco	GELASTOSELTLSOI 	LFIRKSPTITCLVVI
RESULT 1 US-10-723-207-1 Sequence 1. Applicati Publication No. US206 GENERAL INFORMATION: APPLICANT: Wang Cha APPLICANT: Walfield TITLE OF INVENTION: TORIGANISM: NUMBER OF SEQ ID NOG; SOFTWARE: PATCHIN INFORMATION: TYPE: PRT ORGANISM: HUMAN FEATURE: OTHER INFORMATION: OTHER INFORMATION: DUBLICATION INFORMATION: THE INFORMATION: OTHER INFORMATION: OTHER INFORMATION: DUBLICATION INFORMATION: DUBLICATION INFORMATION: OUTHER: INMUNIONING DATE: DUBLICATION INFORMATION: DUBLICATION INFORMATION I	9 90	Qy 310 Db 66	Qy 370

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466 DELTKNQVSLTCLVKGFYPSDIAVEWESN--GQPENNYKTTPPVLDSDGSFFLYSKLTVD 523
                                                                                                                                                                                                  Sequence 8, Application US/11022289;
Publication No. US20050249723A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
TITLE OF INVENTION: F. POLYBEPTIDES WITH NOVEL FC LIGAND BINDING SITES
FILE REPERENCE: 185831/US/2
CURRENT APPLICATION NUMBER: US/11/022,289
CURRENT FILING DATE: 2004-12-21
FRIOR FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.3
SEQ ID NO 8
LENGTH: 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 BPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 GGGSGGGGSFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWSNGQPENNYKTTP
                  --LACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   279 PVLDSDGSFFLYSKLIYUDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSESPGK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     420 TVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           480 DKRT-----LACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 BPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
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                                                                                                             Query Match

49.4%; Score 1513; DB 7;
Best Local Similarity 53.2%; Pred. No. 1.2e-67;
Matches 306; Conservative 47; Mismatches 94;
                                                                                        RAEWEOKDEFICRAVHEAASPSOTVORAVSVNPGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial
                                                                                                                                                                               RESULT 3
US-11-022-289-8
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| Sequence 6, Application US/11022289
| Publication No. US20050249723A1
| GENERAL INFORMATION:
| APPLICANT: Lazar, Gregory Alan
| TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
| FILE REFERENCE: 185831/US/2
| CURRENT APPLICATION NUMBER: US/11/022,289
| CURRENT FILING DATE: 2004-12-21
| PRIOR PILING DATE: 2003-12-22
| NUMBER OF SEQ ID NOS: 15
| SOFTWARE: Patentin version 3.3
| SEQ ID NO 6
| LENGTH: 557
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Matches 306; Conservative
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                                                                                                                                                                                                                                         APPLICANT: Lazar, Gregory Alan
TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
FILE REFERENCE: 186331/US/2
CURRENT APPLICATION NUMBER: US/11/022,289
CURRENT FILING DATE: 2004-12-21
PRIOR FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.3
SEQ ID NO 4

**ENORMAL SECTION NO CONTROL OF THE PATENT OF THE
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; Pred. No. 1.2e-67;
47; Mismatches 100; Indels 122;
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; Publication No. US20050249723A1
; GENERAL INFORMATION:
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Best Local Similarity 53.2
Matches 306; Conservative
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ORGANISM: Artificial
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RESULT 5 US-11-022-289-7

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Sequence 7, Application US/11022289
Publication No. US20050249723A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
TITLE OF INVERTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
FILE REFERENCE: 185831/US/2
CURRENT APPLICATION NUMBER: 2004-12-21
PRIOR APPLICATION NUMBER: US 60/531,752
PRIOR FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.3
SEQ ID NOS: 15
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; Publication No. US20050249723A1
; GENERAL INFORMATION:
; APPLICANT: Last, Gregory Alan
; TITLE OF INVENTION: Fc POLYPEPTIDES WITH NOVEL Fc LIGAND BINDING SITES
; FILE REFERENCE: 185831/US/2
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49.4%; Score 1511; DB 7;
Best Local Similarity 53.4%; Pred. No. 1.5e-67;
Matches 307; Conservative 46; Mismatches 94;
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                                                                                                                                                                                                                                                                                                        TYPE: PRT
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SEQ ID NO 2
LENGTH: 557
TYPE: PRT
ORGANISM: Artificial
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Best Local S:
Matches 304
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Publication No. US20050249723A1
Publication No. US20050249723A1
APPLICAMT: Lazar, Gregory Alan
TITLE OF INVENTION: FC FOLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
FILE REPRENCE: 185831/US/2
CURRENT APPLICATION NUMBER: US/11/022,289
CURRENT FILING DATE: 2004-12-21
PRIOR APPLICATION NUMBER: US 60/531,752
PRIOR FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.3
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53.1%; Pred. No. 1.5e-67;
iive 48; Mismatches 98;
CURRENT APPLICATION NUMBER: US/11/022,289
CURRENT FILING DATE: 2004-12-21
PRIOR APPLICATION NUMBER: US 60/531,752
PRIOR FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIA VERSION 3.3
SEQ ID NO 5
LENGTH: 557
                                                                                                                                                                       OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                                               Matches 306; Conservative
                                                                                                                      TYPE: PRT
ORGANISM: Artificial
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Best Local Similarity
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US-11-022-289-2
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TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
FILE REFERENCE: 185831/US/2
CURRENT APPLICATION VMBER: US/11/022,289
CURRENT APPLICATION NUMBER: US 60/531,752
PRIOR APPLICATION NUMBER: US 60/531,752
PRIOR FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.3
SEQ ID NO
                                                                                 49.3%; Score 1510; DB 7; Length 557;
52.8%; Pred. No. 1.7e-67;
ive 50; Mismatches 98; Indels 124;
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ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic
; OTHER INFORMATION: Synthetic US-11-022-289-2
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301 LSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSA 360
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                    99 EPKSCDKTHTCPPCPAPBLLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                       % Sequence 11, Application US/11022289

§ Sequence 11, Application US/1102289

§ Publication No. US20050249723A1

§ GENERAL INFORMATION:

§ TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES

FILE REPERENCE: 185831/US/2

§ CURRENT APPLICATION NUMBER: US/11/022,289

CURRENT FILING DATE: 2004-12-21

FRIOR APPLICATION NUMBER: US 60/531,752

FRIOR FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 15

§ SOFFWARE: Patentin version 3.3
EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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US-11-022-289-11
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                                                                                                                                                                                                                                                                      361 YLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTL 419
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TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
FILE REFERENCE: 185831/US/2
CURRENT APPLICATION NUMBER: US/11/022,289
CURRENT FILING DATE: 2004-12-21
PRIOR APPLICATION NUMBER: US 60/531,752
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.3
SEQ ID NOS: 15
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                                                                          131;
                                        Length 548;
                                                                        Indels
                                        DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           535 RAEWEQKDEFICRAVHEAASPSQTVQRAVSVNPGK 569
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                                                                          49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/11022289
Publication No. US20050249723A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Synthetic US-11-022-289-10
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Best Local Similarity 52.0%
Matches 298; Conservative
                                                         Best Local Similarity 52.33
Matches 301; Conservative
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ORGANISM: Artificial
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       JS-11-022-289-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 40.0%; Score 1225; DB 7; Length 452; Best Local Similarity 97.0%; Pred. No. 8.4e-54; Matches 225; Conservative 3; Mismatches 4; Indels
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APPLICANT: ZOZULYA, SERGEY
APPLICANT: Kertesz, Nathalie
APPLICANT: Reddy, Ramachandra
APPLICANT: Gill, Parkash
ITTLEANT: Gill, Parkash
ITTLE OF INVENTION: ANGIOGENESIS AND TUMOR GROWTH
ITTLE OF INVENTION: ANGIOGENESIS AND TUMOR GROWTH
FILE REPRENCE: VASG-PO2-002
CURRENT APPLICATION NUMBER: US/10/949,720
CURRENT PILING DATE: 2004-09-23
PRIOR APPLICATION NUMBER: US 60/454,430
PRIOR PILING DATE: 2003-03-12
PRIOR PLING DATE: 2003-03-12
PRIOR PLING DATE: 2003-03-12
PRIOR FILING DATE: 2004-03-12
PRIOR PRIUG DATE: 2004-03-12
PRIOR APPLICATION NUMBER: US 60/454,300
PRIOR PRING DATE: 2004-03-12
PRIOR APPLICATION NUMBER: US 60/454,300
PRIOR APPLICATION NUMBER: US 10/800,350
PRIOR FILING DATE: 2004-03-12
PRIOR FILING DATE: 2004-03-12
PRIOR APPLICATION NUMBER: US 10/800,350
PRIOR FILING DATE: 2004-03-12
PRIOR FILING DATE: 2004-03-12
PRIOR APPLICATION NUMBER: US 10/800,350
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PRIOR FILING DATE: 2004-03-12
PRIOR APPLICATION NUMBER: US 10/800,350
PRIOR FILING DATE: 2004-03-12
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PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: PCT/US00/14142
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/138,133
PRIOR FILING DATE: 1999-06-08
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 390, Application US/10949720 Publication No. US20050249736A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Krasnoperov, Valery
                                                                                                                                                                                                                                                                                                                TYPE: PRT; ORGANISM: Homo sapiens
US-11-016-503-6
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          121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                 219 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Baum, Anke
TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
TITLE OF INVENTION: Chemotherapeutic Agents
TITLE OF INVENTION: Chemotherapeutic Agents
TITLE OF INVENTION: Chemotherapeutic Agents
CURRENT APPLICATION NUMBER: US/11/172,320
CURRENT APPLICATION NUMBER: US/11/172,320
FRIOR FILING DATE: 2003-06-30
FRIOR FILING DATE: 2003-08-21
FRIOR FILING DATE: August 21, 2002
FRIOR FILING DATE: August 22, 2002
FRIOR APPLICATION NUMBER: US 60/405,956
FRIOR FILING DATE: August 26, 2002
FRIOR FILING DATE: August 26, 2002
FRIOR FILING DATE: August 26, 2002
FRIOR FRIOR SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
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TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
TITLE OF INVENTION: AND USING THEREOF
FILE REFERENCE: REG 710-A-US
FURE REFERENCE: REG 710-A-US
CURRENT APPLICATION UNMBER: US/11/016,503
FILE REPLING DATE: 2004-12-17
PRIOR APPLICATION NUMBER: US/10/009,852
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                                                                                                                                                 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                                                                                        279 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
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                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 6, Application US/11172320; Publication No. US20050244413A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 444
TYPE: PRT
ORGANISM: Artificial Sequence
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; Sequence 8, Application US/11016503
; Publication No. US20050245447A1
; GENERAL INFORMATION:
    APPLICANT: Nicholas J. Papadopoulos et al.
    TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED
    TITLE OF INVENTION: MODIFIED CHIMERIC PROPERTIES AND METHODS OF MAKING
    TITLE OF INVENTION: AND USING THEREOF
    TITLE OF INVENTION: AND USING THEREOF
    FILE REFERENCE: REG 710-A-US
    CURRENT APPLICATION NUMBER: US/11/016,503
    CURRENT PILING DATE: 2004-12-16
    PRIOR PELING DATE: 2004-12-16
    PRIOR APPLICATION NUMBER: PCT/US00/14142
    PRIOR APPLICATION NUMBER: 60/138,133
    PRIOR PLING DATE: 1999-06-08
    NUMBER OF SEC ID NOS: 38
    SOFTWARE: FastSEQ for Windows Version 3.0
    SEQ ID NOS: 38
    SEQ ID NOS: 38
    SEQ ID NOS: 38
                    ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                     NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
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Publication No. US20050244410A1
GENERAL INFORMATION:
APPLICANT: Centocor, Inc.
TITLE OF INVENTION: TO11-Like Receptor Binding Agents and Uses Thereof File Reference: CENSO22 USNP
CURRENT APPLICATION NUMBER: US/10/835,475
CURRENT FILING DATE: 2004-04-29
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.2
SEQ ID NO 11
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ORGANISM: Homo sapiens
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Matches 225; Conserv
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US-10-835-475-11
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                                                                                                                                                                Gaps
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TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Predicted Mature Form of TLR9 EC260-Fc Fusion
US-10-835-475-11
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                                                                                                                    Query Match
40.0%; Score 1225; DB 1; Length 489;
Best Local Similarity 96.1%; Pred. No. 9e-54;
Matches 224; Conservative 5; Mismatches 4; Indels
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Sequence 176, App
Sequence 176, App
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Sequence 34, Appli
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Sequence 37, Appl
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-10-627-556-184

US-10-627-556-189

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	SULT 1 -09-847-208-7 Sequence 7, Application US/09847208 Bublication No. US20030082190A1 GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Saxon, Andrew APPLICANT: Saxon, Andrew APPLICANT: Shang, Ke APPLICANT: Shang, Ke APPLICANT: Chang, Ke CURRENT FILING DATE: 2001-05-01 NUMBER OF SEQ ID NOS: 177 SOFTWARE: FastSEQ for Windows Version 4.0 LENGTH: 569 LENGTH: 569 LENGTH: SF CREANTES: OFTHER INFORMATION: (IGE) CHER INFORMATION: (IGE)	-7 100.0%; Score 3060; DB 3; Length 569; Similarity 100.0%; Pred. No. 5.5e-193; Conservative 0; Mismatches 0; Indels 0; Gaps EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVUDVSHEDPEVKF.	NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
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DD 361 YLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLT 420 421 VTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRD 480	RESULT 3 US-10-047-542-45 US-10-047-542-45 Sequence 45, Application US/10047542 Fublication No. US20020168367A1 GENERAL INFORMATION. THILE OF INVENTION. TITLE OF INVENTION: AND BACTERIAL DISEASES FILE REPERENCE: 030905.0004.CIP1 CURRENT APPLICATION NUMBER: VG/10/047,542 CURRENT APPLICATION NUMBER: PCT/US01/13932 FRIOR FILING DATE: 2001-10-26 FRIOR APPLICATION NUMBER: FCT/US01/13932 FRIOR FILING DATE: 2001-04-28 FRIOR FILING DATE: 2000-04-28 FRIOR FRIOR FRIOR DATE: 2000-04-28 FRIOR FRIOR PARTER DATE DATE DATE DATE DATE DATE DATE DATE	Query Match 58.0%; Score 1775; DB 4; Length 574; Best Local Similarity 77.3%; Pred. No. 2e-108; Matches 351; Conservative 17; Mismatches 60; Indels 26; Gaps 8; Qy 120 TISKAVQPREPQVYILPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 177	178 200 236 252		Qy 416 NGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEW 475 Db 421 NGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEW 480 Qy 476 PGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTR 535 Db 481 PGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTR 540 Qy 536 ABWEQKDEFICRAVHEAASPSQTVQRAVSVNPGK 569 Qy 536 ABWEQKDEFICRAVHEAASPSQTVQRAVSVNPGK 569
Db 301 LSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRCVSA 360	Qy 541 KDEFICRAVHEAASPSQTVQRAVSVNPGK 569	; FEATURE: ; OTHER INFORMATION: Fusion polypeptide comprising a hinge-CH2-CH3 ; OTHER INFORMATION: (IgG1) sequence and a CH2-CH3-CH4 (IgE) sequence US-10-000-439-7 Query Match Best Local Similarity 100.0%; Score 3060; DB 4; Length 569; Best Local Similarity 100.0%; Pred. No. 5.5e-193; Matches 569; Conservative 0: Mismatches 0: Indels 0: Gaps 0:	CCPPCPAPELLGGPSVFLPPFKDTLMISRTPSVTCVVDVSHEDPBVKF 60 [[121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP	OY 241 GGGSGGGGSFTPPTVKILQSSCDGGGHPPFIQLLCLVSGYTPGTINITWLEDGQVMDVD 300

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                                                                        Sequence 37, Application US/10214524

Sequence 37, Application US/10214524

Publication No. US20030073142A1

GENERAL INPORMATION:

APPLICANT: Yang, Yong-Min

APPLICANT: Barankiewicz, Theresa J.

APPLICANT: Chen, Zhong

TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF

TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF

TITLE OF ILVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF

TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS

TITLE OF INVENTION NUMBER: 60/312,120

PRIOR PILING DATE: 2001-08-08

NUMBER OF SEQ ID NOS: 61

SOFTWARE: Patentin version 3.1

SEQ ID NO 37
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541 AEWEQKDEFICRAVHEAASPSQTVQRAVSVNPGK 574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Renner, Wolfgang A. APPLICANT: Bachmann, Martin APPLICANT: Tissot, Alain MarpLICANT: Maurer, Parick APPLICANT: Lechner, Franziska
                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Human (Homo sapiens)
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 58.0
Best Local Similarity 77.3
Matches 351; Conservative
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US-10-050-902-176
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120 IISKAKVQPREPQVYTLPPSRDELTKNQVSLT--CLVKGFYPSDIAVEWESNGQPENNYK 177
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APPLICANT: SCHOLL, FOLGE, APPLICANT: SCHOLL, APPLICANT: SCHOLL, SCHOLL APPLICANT: PLOSSEK, Christine
TITLE OF INVENTION: Molecular Antigen Array
FILE REFERENCE: 1700.0190004
CURRENT APPLICATION NUMBER: US 60/262,379
PRIOR PILING DATE: 2001-01-9
PRIOR FILING DATE: 2001-05-04
PRIOR PLICATION NUMBER: US 60/286,998
PRIOR PLICATION NUMBER: US 60/326,998
PRIOR PLING DATE: 2001-10-05
PRIOR PLING DATE: 2001-10-05
PRIOR PLING DATE: 2001-10-05
PRIOR PLING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 350
SOFTWARE: PATENTIN VET: 2.1
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APPLICANT: Bachmann, Martin
APPLICANT: The Soct, Alain
APPLICANT: Lechner, Franziska
APPLICANT: Lechner, Franziska
APPLICANT: Piossek, Christine
APPLICANT: Ortmann, Rainer
APPLICANT: Luond, Rainer
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420 475 480 535

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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 5
LENGTH: 427
                                         TYPE: PRT
CORGANISM: Homo sapiens
US-09-847-208-5
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US-10-000-439-5
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Publication No. US20030082190A1

GENERAL INFORMATION:
APPLICANT: Zhang, Ke

APPLICANT: Zhang, Ke

APPLICANT: Zhang, Ke

TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF

TITLE OF INVENTION: 1gg-Mediated ALLERGIC DISEASES

FILE REFERENCE: UC67.002A

CURRENT APPLICATION NUMBER: US/09/847,208

CURRENT FILING DATE: 2001-05-01

NUMBER OF SEQ ID NOS: 177
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     Staufenbiel, Matthias
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ORGANISM: IGE heavy chain

US-10-050-898-176
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  Length 427;
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APPLICANT: Saxon, Andrew
TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR; TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES; FILE REFERENCE: UC067.004A; CURRENT APPLICATION UNMERR: US/10/000,439; CURRENT FILNG DATE: 2001-10-24; PRIOR APPLICATION NUMBER: US 09/847,208; PRIOR FILING DATE: 2001-05-01
Query Match 57.7%; Score 1766; DB 3; Best Local Similarity 78.0%; Pred. No. 5.6e-108; Matches 347; Conservative 17; Mismatches 57;
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57.7%; Score 1766; DB 4;
Best Local Similarity 78.0%; Pred. No. 5.6e-108;
Matches 347; Conservative 17; Mismatches 57;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
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224 PSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTST 283
                                                        485 ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEF
                                   LPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL
                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09949375A
; Batent No. US20020172673A1
; GENERAL INFORMATION:
; APPLICANT KIYSNER, Steen et al.
; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
; FILE REFERENCE: 3631-0111P
; CURRENT APPLICATION NUMBER: US/09/949,375A
; CURRENT FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
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OTHER INFORMATION: Human 19E heavy chain C3 domain
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OTHER INFORMATION: Human 1gE heavy chain C1 domain
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NAME/KEY: MISC_FEATURE
LOCATION: (209)..(216)
OTHER INFORMATION: Linker between domains
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OTHER INFORMATION: Linker between domains
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OTHER INFORMATION: Epitope in DE loop
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LOCATION: (301)...(311)
OTHER INFORMATION: Epitope in FG loop
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INFORMATION: Human 1gE heavy
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LOCATION: (205)..(219)
OTHER INFORMATION: Epitope
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LOCATION: (315)..(323)
OTHER INFORMATION: Epitope
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LOCATION: (244)..(251)
OTHER INFORMATION: Epitope
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ORGANISM: homo sapiens
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US-09-949-375A-1
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     186 VGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY-QQRSLSLSPGKVEGGGGGGGGG 244
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Fatent No. US2002046422A1

GENERAL INFORMATION:

APPLICANT: Bachmann, Martin F.

APPLICANT: Bachmann, Martin F.

TITLE OF INVENTION: Compositions for Inducing Self-Specific Anti-IgE

TITLE OF INVENTION: Antibodies and Uses Thereof

TITLE OF INVENTION: Antibodies and Uses Thereof

FILE REFERENCE: 1700.014001

CURRENT APPLICATION NUMBER: US/09/916,230

CURRENT FILING DATE: 2001-07-27

FRIOR PELLOR OF SEQ ID NOS: 35

NUMBER OF SEQ ID NOS: 35

SOFTWARE: Patentin version 3.0

SEQ ID NO. 1005: 35
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                         62 SGHYATISLLTV-SGAWAK-QMFTCRVAHTPSSTDWVDNKTFSVC---
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ORGANISM: Homo sapiens
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                                           63 SGHYATISLITV-SGAWAK-QMFTCRVAHTPSSTDWVDNKTFSVC---
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TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
FILE REFERENCE: 4614-0115P
CURRENT APPLICATION NUMBER: US/10/363,954A
CURRENT FILING DATE: 2003-03-06
PRIOR APPLICATION NUMBER: US 60/232,831
PRIOR APPLICATION NUMBER: DK PA 2000 01326
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-16
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
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OTHER INFORMATION: Epitope including C2C3 linker
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OTHER INFORMATION: Epitope including C3C4 linker
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OTHER INFORMATION: Linker between domains C2
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OTHER INFORMATION: Human IgE heavy chain reature:
NAME/KEY: MISC FEATURE
LOCATION: (209)
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OTHER INFORMATION: Epitope in DE loop
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OTHER INFORMATION: Epitope
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NAME/KEY: MISC_FEATURE
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Sequence 60, Application US/10047542

Publication No. US20020168367A1

SEQUENCE 60, Application NO. US20020168367A1

APPLICANT: LARRICK, JAMES W.

APPLICANT: WINCOFF, KEITH L.

TITLE OF INVENTION: NOVEL INMUNOADHESINS FOR TREATING AND PREVENTING VIRAL

TITLE OF INVENTION: AND BACTERIAL DISEASES

FILE REPREMENCE: 030905.0004.CIPL

CURRENT APPLICATION NUMBER: US/10/047,542

CURRENT FILING DATE: 2001-10-26

PRIOR FILING DATE: 2001-04-28

PRIOR FILING DATE: 2001-04-28

PRIOR FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 101

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 60
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                                                                                          Length 428;
                                                                                                                                          57; Indels
                ; OTHER INFORMATION: Human IgE heavy chain C2 domain US-09-949-375A-1
                                                                                          57.7%; Score 1766; DB 3; 78.0%; Pred. No. 5.6e-108;
                                                                                          Query Match
57.7%; Score 1766; DI
Best Local Similarity 78.0%; Pred. No. 5.6e
Matches 347; Conservative 17; Mismatches
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Best Local Similarity 78.01
Matches 347; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Homo sapiens
US-10-047-542-60
  LOCATION: (113) .. (208)
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ORGANISM: homo sapiens
                               FEATURE:
NAME/KEY: DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 SGHYATISLLTV-SGAWAK-OMFTCRVAHTPSSTDWVDNKTFSVC--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTST
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            24;
                                                                                                                                                                                                                                                                                                                                                                     Query Match
57.7%; Score 1766; DB 4; Length 428;
Best Local Similarity 78.0%; Pred. No. 5.6e-108;
Matches 347; Conservative 17; Mismatches 57; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/09949375A; Patent No. US20020172673A1; GENERAL INFORMATION:
APPLICAMT: KLYSNER, Steen et al.
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE; FILE REFERENCE: 3631-0111P; CURRENT APPLICATION NUMBER: US/09/949,375A; CURRENT FILING DATE: 2002-01-18; NUMBER OF SEQ ID NOS: 38; SOFTWARE: Patent In version 3.1; SEQ ID NO 7
                                                                                                                   ^{\circ}_{2}
                                                                                                                                                                                                                                                                                                    ; LOCATION: (113)..(208)
; OTHER INFORMATION: Human IgE heavy chain C2 domain US-10-363-954A-1
                                                                 FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (317) . (320)
OTHER INFORMATION: Linker between domains C3 and
                                                                                                                                                                    LOCATION: (321)...(422)
OTHER INFORMATION: Human 19E heavy chain C4
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                                                                                                                                                                                                                      NAME/KEY: DOMAIN
LOCATION: (217)...(316)
OTHER INFORMATION: Human IGE heavy chain
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                                   LOCATION: (301)..(311)
OTHER INFORMATION: Epitope in FG loop
       MISC FEATURE (301)..(311)
                                                                                                                                                                                                                                                                                         NAME/KEY: DOMAIN
                                                                                                                                                    NAME/KEY: DOMAIN
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FEATURE:
NAME/KEY: N
LOCATION:
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LENGTH: 441

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129 REPQUYTLPPSRDELIKNQVSLT--CLVKGFYPSDIAVEWESNGQPENNYKTTP-PVLDS 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MISC FEATURE
LOCATION: (205)..(219)
OTHER INFORMATION: Epitope including C2C3 linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (3157..(323)
OTHER INFORMATION: Epitope including C3C4 linker
LOCATION: (11)...(106)
OTHER INFORMATION: IGE heavy chain Cl domain
                                                                                                                                                                                                                                                                  LOCATION: (321)...(422)
OTHER INFORMATION: IGE heavy chain C4 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between domains C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (318)..(320)
OTHER INFORMATION: Linker between domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: MISC FEATURE
LOCATION: (301)...(311)
COTHER INFORMATION: Epitope in FG loop
US-09-949-375A-7
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OTHER INFORMATION: Epitope in BC loop
                                                                                                          heavy chain
                                                                                                                                                                                               chain
                                                                                                                                                                                                                                                                                                                                                       LOCATION: (427)..(441)
OTHER INFORMATION: MIGIS fragment
                                                                                                                                                                                               heavy
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Best Local Similarity 77.9%
Matches 345; Conservative
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OTHER INFORMATION: Epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Linker
                                                                                     LOCATION: (113)..(208)
OTHER INFORMATION: IGE
                                                                                                                                                                          LOCATION: (217)..(317)
OTHER INFORMATION: IGE
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RESULT 15
US-10-872-932A-35
US-10-872-932A-35
Sequence 35, Application US/10872932A
Sequence 35, Application No. US2050033029A1
GENERAL INFORMATION:
APPLICANT Jin Lu
TILLE OF INVENTION:
FILE REFERENCE: CENSO31NP
CURRENT FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: US/10/872,932A
CURRENT FILING DATE: 2004-06-21
PRIOR FILING DATE: 2004-06-21
SPRIOR APPLICATION NUMBER: US 60/483,654
SOFTWARE: Patentin Version 3.3
SOFTWARE: Patentin Version 3.3
LENGTH: 497
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                                                                                                                                                                                                                                                                                                                                                                                                                    62
                                                                                                                                                                                                                                                                                                                                                                                                  305 STTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSR
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Best Local Similarity 77.9%; Pred. No. 3.1e-107;
Matches 345; Conservative 17; Mismatches 57;
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                    LOCATION: (244)..(251)
OTHER INFORMATION: Epitope in BC loop FEATURE.
NAME/KEY: MISC FEATURE
LOCATION: (272)..(280)
OTHER INFORMATION: Epitope in DE loop FEATURE.
NAME/KEY: MISC FEATURE
LOCATION: (301)..(311)
OTHER INFORMATION: Epitope in FG loop
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    NAME/KEY: MISC FEATURE LOCATION: (244)..(251)
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LPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL
                                                                                                                                                        485 ACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEF
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/10363954A

Publication No. US20040156838A1

GENERAL INFORMATION:
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE

FILE REFERENCE: 4614-0115P

CURRENT APPLICATION NUMBER: US/10/363,954A

CURRENT FILING DATE: 2003-03-06

PRIOR PAPLICATION NUMBER: US 60/232,831

PRIOR PLICATION NUMBER: US 60/232,831

PRIOR FILING DATE: 2000-09-15

PRIOR FILING DATE: 2000-09-06

NUMBER OF SEQ ID NOS: 38

SOFTWARE: PatentIn version 3.1
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NAME/KEY: MISC_FEATURE
LOCATION: (318)..(320)
OTHER INFORMATION: Linker between domains C3 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (209)...(216)
OTHER INFORMATION: Linker between domains C2 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (205)..(219)
OTHER INFORMATION: Epitope including C2C3 linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MISC_FEATURE
LOCATION: (315)..(323)
OTHER INFORMATION: Epitope including C3C4 linker
FRAMURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: DOMAIN
LOCATION: (321)..(422)
OTHER INFORMATION: IgE heavy chain C4 domain
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OTHER INFORMATION: IGE heavy chain C1 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (113)...(208)
OTHER INFORMATION: 19E heavy chain C2 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain
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OTHER INFORMATION: IGE heavy chain C3
                                                                                                                                                                                                                                                                       404 ICRAVHEAASPSQTVQRAVSVNP 426
                                                                                                                                                                                                                                            545 ICRAVHEAASPSQTVQRAVSVNP 567
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LOCATION: (427)..(441)
JTHER INFORMATION: MIGIS fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
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NAME/KEY: DOMAIN
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NAME/KEY: DOMAIN
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129 REPOVYTLPPSRDELTKNOVSLT -- CLVKGFYPSDIAVEWESNGOPENNYKTTP-PVLDS 185
                  186 VGSFFLYSKLTYDKSRWQQGNVFSCSVMHEALHNHY-QQRSLSLSLSBGKVEGGGGGGGGG 244
                         4 QSPSVFPLTRCCKNIPSNATSVTLGCLATGYFPEPVMVTWDT-GSLNGTTWTLPATTLTL 62
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Search completed: November 30, 2005, 00:46:36 Job time : 170 secs

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1 EPKSCDKTHTCPPCPAPELL.....HEAASPSQTVQRAVSVNPGK
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(c) 1993 - 2005 Compugen Ltd.
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geneseqp20028:* geneseqp2003as:* geneseqp2003bs:* geneseqp20048:* geneseqp20058:*

geneseqp2000s:*geneseqp2001s:* geneseqp1990s:*

Database

	Description	Aao19668 GE2 fusio	Abg94250 Human IgE	Human	Human	Human	Human	Aam47863 Human Ig-	Aau80283 Human IgE	Aam50940 Human IgE	Human	Human	Ade97382 Human IgE	Aap40065 Sequence		Adw24784 Human var		Adz08809 Mammalian	Adz08940 Mammalian	Adz44466 Human imm		Aeb72776 Anti-LTal			Ady21754 Antibody
SUMMARIES	ID	AA019668	ABG94250	ABG80562	ABP96592	ADE97368	AA019666	AAM47863	AAU80283	AAM50940	AAE35113	ADD48440	ADE97382	AAP40065	AAU80287	ADW24784	ADW24742	ADZ08809	ADZ08940	ADZ44466	AEA16541	AEB72776	ADY22009	ADD25773	ADY21754
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	Score		1775	1775	1775	1775	1766	1766	1766	1766	1766	1766	1766	1760	1755	1754.5	1754.5	1754.5	1754.5	1754.5	1754.5	1754.5	1733.5	1729	72
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ADY21805	ADY21809	ADY21801	AAR42950	ADY21873	AAE35114	3 AAO19667	. AAU80286	. AAU80285	3 AAU80284	AAR83559	3 AAR75225	AAR77241	9 ADY21849	3 AAB03642	7 ADD25768	9 ADY21799	ADY21722	L AAP80291	5 ABP96581	3 AAY79994
648 9	648 9	635	428 2	593	425	320	323 5	323 5	323 5	324	325 2	325	327	331	331	331	331	367	426	325
56.4	56.4	56.4	56.3	56.3	56.2	55.8	55.8	55.8	55.8	55.8	55.8	55.8	55.8	55.8	55.8	55.8	55.8	55.8	55.7	55.6
1727	1725.5	1725	1723	1721.5	1720.5	1707	1707	1707	1707	1707	1707	1707	1707	1707	1707	1707	1707	1707	1705.5	1701
25	5	27	20	50	0.6	31	32	33	34	35	36	37	38	6 6	40	41	42	4.3	44	45

ALIGNMENTS

Human, IGE; immunoglobulin E; immunotherapy; immune disease; Fcepsilon receptor; autoimmune disease; constant region; heavy chain; antiasthmatic; antiallergic; antiinflammatory; dermatological; GE2; antiarthritic; antirheumatic; antidiabetic; neuroprotective; GE2 fusion protein for use in treating immune diseases. AA019668 standard; protein; 569 AA 01-MAY-2002; 2002WO-US013527 01-MAY-2001; 2001US-00847208. 24-OCT-2001; 2001US-00000439. ä (first entry) (REGC) UNIV CALIFORNIA. Zhu WPI; 2003-103456/09. Zhang K, WO200288317-A2. fusion protein. Synthetic. Unidentified. 28-MAR-2003 07-NOV-2002 AA019668; Saxon A, AA019668

New fusion molecules comprising polypeptide sequences that bind to IgG inhibitory receptor and native IgE receptor, useful for treating IgE-mediated hypersensitivity reactions, e.g. asthma or allergies, or autoimmune diseases.

Claim 35; Fig 7; 116pp; English.

The present invention relates to a fusion molecule comprising a first polypeptide sequence capable of specific binding to a native IgG inhibitory receptor consisting of an immune receptor tyrosine-based inhibitory motif (ITIM), expressed on mast cells, basophils or B cells, functionally connected to a second polypeptide sequence capable of specific binding directly or indirectly to a native IgE receptor

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ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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(FcepsilonR). Also provided are nucleotide sequences encoding such a fusion protein. The fusion melecules and compositions are useful for treating an IgE-mediated biological response, preferably an IgE-mediated hypersensitivity reaction, such as asthma, allergic rhinitis, atopic dermatitis, severe food allergies, chronic urticaria, angioedema or anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis, type-I diabetes mellitus, or multiple sclerosis, and for preventing of, or symptoms resulting from, a type I hypersensitivity reaction in a subject receiving immunotherapy. The present sequence is a gammahinge-CHgamma2-CHgamma2-(CHepsilon2-CHepsilon3-CHepsilon3 fusion protein (designated GE2) of the invention
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                                                                                                                                                                                                                                                                                                                                                                            EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGKVEGGGGSG
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                                                                                                                                                                                                                                                                                              Best Local Similarity
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Molecular antigen array used in the production of vaccines for infectious

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Sebbel

Lechner F,

Maurer P,

Bachmann M, Tissot A,

Renner WA,

Piossek C;

WPI; 2002-627351/67.

CYTO-) CYTOS BIOTECHNOLOGY AG

19-JAN-2001; 2001US-0262379P. 04-MAY-2001; 2001US-0288549P. 05-OCT-2001; 2001US-0331045P. 07-NOV-2001; 2001US-0331045P.

21-JAN-2002; 2002WO-IB000166

WO200256905-A2

25-JUL-2002

Homo sapiens.

Synthetic.

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                                                                                                                                                                                   Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory; cytostatic; antiviral; antidiabetic; hypoglycaemic; antigen array; vaccine; infectious disease.
                                                                                                                                                   Human IgE heavy chain constant region peptide #1
                                   ABG94250 standard; protein; 574 AA.
                                                                                                             (first entry)
                                                                                                               10-DEC-2002
                                                                         ABG94250;
                 ABG94250
RESULT
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This invention relates to a novel ordered and repetitive antigen array used in the production of vaccines for infectious diseases. The invention also discloses a composition comprising a non-natural molecular scaffoold comprising a core particle selected from a core particle of natural origin and a core particle of natural origin and an organiser comprising at least one first attachment site, where the organiser is connected to the core particle by at least one covalent bond. Also disclosed is an antigen or antigenic determinant with at least one second attachment site, where the antigen or antigenic determinant site not naturally occurring with the antigenic determinant site not naturally occurring with the antigenic determinant site not naturally occurring with the antigenic determinant is an attachment site and where the antigen or antigenic determinant, where the second attachment site is capable of association through at least one non-peptide bond to the first attachment site and where the antigen or antigenic determinant and the scaffold interact through the association to form an ordered and repetitive antigen array. The invention also comprises a cost proteins capable of forming a capsid which comprises mutant Obeta cost proteins having an amino acid sequence selected from five amino acid sequences thilly defined in the specification. The compounds of the invention may the artification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 TISKAKVQPREPQVYTLPPSRDELTKNQVSLT--CLVKGFYPSDIAVEWESNGQPENNYK 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunisation and as a vaccine. The present sequence represents a protein sequence used to create the compositions of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        have antimicrobial, antiallergic, immunomodulatory, cytostatic, antiviral, antidiabetic, or hypoglycaemic activities and may be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 TTP-PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY-QQRSLSLSPGKVEG
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Matches 351; Conservative
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ABP96592 standard; protein; 574
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                                                                                                                                                                                                                                                      Molecular antigen array; vaccine; antigen; antimicrobial; molecular scaffold; amyloid beta; Abeta 1-42; influenza; graft versus host disease; IgE-mediated allergic reaction; anaphylaxis; adult respiratory distress syndrome; ARDS; Crohn's disease; allergic asthma; acute lympholastic leukaemia; non-Hodgkin's lymphoma; Grave's disease; systemic lupus erythematosus; osteoporosis; imflammatory immune disease; myasthenia gravis; multiple sclerosis; immunoproliferative disease lymphadenopathy; Alzheimer's disease; angioimmunoproliferative lymphadenopathy; immunoblastive lymphadenopathy; rheumatoid arthritis; diabetes; infectious disease; factor Xa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccines for infectious
         540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a composition comprising: (a) a non-natural molecular scaffold comprising: (i) a core particle selected from: (l) a
                                                                                 NGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEW
                                                                       PGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTR
RGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQR
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Piossek C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecular antigen array used in the production of
                                                                                                                        ਲ, D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lueoend F
Sebbel F
                                                                                                                                                                                                                                                                                                                                                       enterokinase; cysteine-containing linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 366-368; 418pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ortmann R,
Tissot A,
                                                                                                                                                                                ABG80562 standard; protein; 574 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOS BIOTECHNOLOGY AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JAN-2001; 2001US-0262379P.
04-MAY-2001; 2001US-0288549P.
05-OCT-2001; 2001US-032699RP.
07-NOV-2001; 2001US-0331045P.
                                                                                                                                                                                                                                                                                                                                                                                                                                21-JAN-2002; 2002WO-IB000168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOVARTIS PHARMA AG.
MAURER P.
                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bachmann M,
                                                                                                                                                                                                                                      Human IgE heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STAUFENBIEL FREY P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-636514/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lechner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LECHNER F.
ORTMANN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LUEOEND
                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                     29-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                             25-JUL-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maurer P,
Renner WA,
                                                                                                                                                                                                  ABG80562;
                                     416
                                                       421
                                                                                            481
                                                                                                               536
                                                                          476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LECH/)
(ORTM/)
(LUEO/)
(STAU/)
(FREY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CYTO-)
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                                                                                                                                                              RESULT 3
                                                                                                                                                                        ABG80562
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core particle of a non-natural origin; and (2) a core particle of natural coign; and (ii) an organiser is connected to the core particle by at least one covalent bond; (b) an antigen or antigenic determinant with at least one covalent bond; (b) an antigen or antigenic determinant with at least one second attachment site; where the antigen or antigenic determinant is attachment site is selected from: (i) an attachment, and where the second attachment site not naturally occurring with the antigen or antigenic determinant; where the second attachment site is capable of association through at least one non-peptide bond to the first attachment site; and where the association of through at least one non-peptide bond to the first attachment site; and where the antigen or antigenic determinant and the scaffold interact through the association to form an ordered and repetitive antigen or antigenic determinant and the scaffold interact through the association to form an ordered and repetitive antigen array. The composition is used in construction and as a vaccine for disease such as influenza, graft or immunisation and as a vaccine for disease such as influenza, graft versus host disease, IgE-mediated allergic reactions, anaphylaxis, adult correct through attribute and allergic reactions, anaphylaxis, acute laymanatory distress syndrome (ARDS), Crohn's disease, allergic asthma, correct laymanobastic letakemia, non-Hodgkin's lymphoma, Grave's disease, cargioimmunoproliferative lymphadenopathy, immunoblastic latekemia, non-Hodgkin's lymphoma, Grave's disease, captoimmunoproliferative lymphadenopathy, immunoblastic latekemia, non-Hodgkin's lymphoma, Grave's disease, captoimmunoproliferative lymphadenopathy, immunoblastic latekemia, non-Hodgkin's lymphoma, Grave's disease, congroimmunoproliferative lymphadenopathy, immunoblastic latekemia, non-Hodgkin's lymphoma, grave's disease, congroimmunoproliferative lymphadenopathy, and antigen conference of concerninal linker peptide which serves as the attachment point to a cleavage 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   æ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTP-PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY-QQRSLSLSPGKVEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 GGGSGGGGGGGFTPPTVKILQSSCDGGGHPPPTIQLLCLVSGYTPGTINITWLEDGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VMDVDLSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 TVSSASTQ--SPSVFPLTRCCKNIPSNATSVTLGCLATGYFPEPVMVTWDT-GSLNGTTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

58.0%; Score 1775; DB 5;
Best Local Similarity 77.3%; Pred. No. 5.6e-114;
Matches 351; Conservative 17; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 574 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178
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Identifying peptides that induce cytotoxic T-lymphocyte, CTL response against IgE, by identifying peptide eliciting CTL response to IgE peptides naturally presented by major histocompatibility complex class I
                                                                       antiallergic; antiasthmatic; immunosuppressivė; vasotropic; cytostatic; dermatological; antiinflammatory; IGE-mediated condition; food allergy; atopic hypersensitivity condition, allergic rhinitis; allergic asthma; atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
                                                            response; major histocompatibility complex; MHC; immunogenic;
                                                   Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response;
                             Human IgE heavy chain amino acid sequence SEQ ID NO:37.
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                                                                                                                                                                                                                                                               Chen
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                                                                                                                                                                                                                                                                 Barankiewicz
                                                                                                                                                                                                                      13-AUG-2001; 2001US-0312120P.
                                                                                                                                                                                                 08-AUG-2002; 2002WO-US026986
                                                                                                                                                                                                                                           (IGET-) IGE THERAPEUTICS INC
        (first entry)
                                                                                                                                                                                                                                                                                   WPI; 2003-268242/26.
                                                                                                                                                                                                                                                               Yang Y,
                                                                                                                 urticaria hives.
                                                                                                                                                         WO2003015716-A2
                                                                                                                                     Homo sapiens
         28-MAY-2003
                                                                                                                                                                             27-FEB-2003
                                                                                                                                                                                                                                                                 Chen SA,
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Example 7; Page 174-177; 187pp; English.

protein

The present invention describes a method (M1) for identifying peptides that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin CE [1gE], comprising providing a test peptide (T) suspected of being able to bind to major histocompatibility complex (MHC) class I molecule, and cavaluating (T) for ability to elicit in a mammal a CTL response to canturally processed and presented 1gE peptides, where a peptide that induces such a response is identified. Also described are compositions: (C1) comprising at least one immunogenic peptide (I) identified by (M1); (C2) comprising at least one immunogenic peptide (I) identified by (M1); (C2) comprising at least one isolated polynuclosotide encoding (I); and (C3) comprising antigen-presenting cells that recognise at least one (I) Where C1-3 are able to bind to at least one MHC class I molecule and to calcif in a mammal and to naturally processed and presented (G2) comprising antigen-presenting cells that recognise at least one (I) where C1-3 are able to bind to at least one attractive, and can be used as inducers of a CTL response against 1gE, and in a cand can be used as inducers of a CTL response against 1gE, and in a correction such as allergic mammal. C1-3 are useful for modulating an 1gE-mediated condition in a mammal. C1-3 are useful for modulating an 1gE-mediated condition in a cuseful for treating atopic hypersensitivity conditions (such as allergic confining, allergic atopic hypersensitivity conditions (such as allergic atopic hypersensitivity conditions (such as anaphylaxis, and urticaria chives). The present sequence represents an 1gE heavy chain amino acid sequence, which is given in an example from the present invention

Sequence 574 AA;

Gaps 60; Indels 26; Length 574; 58.0%; Score 1775; DB 6; 77.3%; Pred. No. 5.6e-114; ive 17; Mismatches 60; Best Local Similarity 77.3 Matches 351; Conservative Query Match

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TTP-PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY-QQRSLSLSPGKVEG 235 178

295 300 355 360 415 420 475 480 535 540 251 OSET THE TOTAL T 200 TLPATTLTLSGHYATISLLTV-SGAWAK-QMFTCRVAHTPSSTDWVDNKTFSVC----GGGSGGGGGGGSFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQ VMDVDLSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNP 301 VMDVDLSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNP 361 RGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEBKQR NGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEW PGSRDKRTLACLIONFMPEDISVOWLHNEVOLPDARHSTTOPRKTKGSGFFVFSRLEVTR RGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQR PGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTR 541 AEWEQKDEFICRAVHEAASPSQTVQRAVSVNPGK 574 AEWEQKDEFICRAVHEAASPSQTVQRAVSVNPGK 476 481 296 356 416 252 536 RESULT 5 셤 g d g g g 8 ò 8 8 ò ò

ADE97368 standard; protein; 574 12-FEB-2004 ADE97368;

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immunoadhesin; immunoglobulin heavy chain; J chain; joining; toxin; virucide; antibacterial; anthrax; rhinovirus infection; common cold; intercellular adhesion molecule; ICAM-1; human. Human immunoadhesin-related protein - SEQ ID 45.

WO2003064992-A2 sapiens. Homo

25-OCT-2002; 2002WO-US034197.

07-AUG-2003

26-OCT-2001; 2001US-00047542.

(PLAN-) PLANET BIOTECHNOLOGY INC. LARRICK J W. (WYCO/) WYCOFF K L. (LARR/)

ij

Larrick JW, Wycoff

WPI; 2003-636816/60.

New immunoadhesin, useful for treating anthrax and rhinovirus, comprises chimeric toxin receptor protein linked to immunoglobulin heavy chain, and J chain and secretory component associated with the chimeric toxin receptor protein.

Disclosure; SEQ ID NO 45; 288pp; English

toxin receptor protein consisting of a toxin receptor protein linked to at least a portion of an immunoglobulin heavy chain with a J (joining) chain and secretory component (SC) associated with the chimeric toxin receptor protein. The immunoadhesin comprises a chimeric bacterial or viral toxin receptor protein and the immunoadhesin has plant-specific glycosylation. The immunoadhesin of the invention demonstrates virucide The invention relates to a novel immunoadhesin comprising a chimeric

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                                                                                                         TISKAKVQPREPQVYTLPPSRDELTKNQVSLT--CLVKGFYPSDIAVEWESNGQPENNYK 177
                                                                                                                                                             251
and antibacterial activities and may be useful for reducing the binding of a viral or bacterial antigen to a host cell and thus for treating or preventing anthrax, as well as human rhinovirus infection which results in the common cold. The current sequence is that of the human immunoadhesion-related protein of the invention.
                                                                                                                   -----SRDFTPPTVKILQSSCDGGGHPPPTIQLLCLVSGYTPGTINITWLEDGQ
                                                                                                                                                                                                                            TTP-PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY-QQRSLSLSPGKVEG
                                                                                                                                                       GGGSGGGGGGGFTPPTVKILQSSCDGGGHPPPTIQLLCLVSGYTPGTINITWLEDGQ
                                                                                                                                                                                                                  VMDVDLSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNP
                                                                                                                                                                                                                                                     RGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQR
                                                                                                                                                                                                                                                                                         NGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEW
                                                                                                                                                                                                                                                                                                  PGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; IgE; immunoglobulin E; immunotherapy; immune disease; Fcepailon receptor; autoimmune disease; constant region; heavy antiasthmatic; antiallergic; antiinflammatory; dermatological; antiarthritic; antirheumatic; antidiabetic; neuroprotective.
                                                                                         26;
                                                                      Length 574;
                                                                                        60; Indels
                                                                      58.0%; Score 1775; DB 7; 77.3%; Pred. No. 5.6e-114; ive 17; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                              569
                                                                                                                                                                                                                                                                                                                                                             AEWEQKDEFICRAVHEAASPSQTVQRAVSVNPGK
                                                                                                                                                                                                                                                                                                                                                                        Human IgE heavy chain constant region.
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                                                                                                                                                                                                                                                                                                                                                                                                                           AAO19666 standard; protein; 427
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24-OCT-2001; 2001US-00000439.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                         Matches 351; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (REGC ) UNIV CALIFORNIA.
                                                                                 Similarity
                                                       Sequence 574 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200288317-A2
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The present invention relates to a fusion molecule comprising a first polypeptide sequence capable of specific binding to a native IgG inhibitory receptor consisting of an immune receptor tyrosine-based inhibitory motif (ITIM), expressed on mast cells, basophils or B cells, functionally connected to a second polypeptide sequence capable of specific binding directly or indirectly to a native IgE receptor (Ecopsilons). Also provided are nuclectide sequences encoding such a fusion protein. The fusion molecules and compositions are useful for treating an IgE-mediated biological response, preferably an IgE-mediated by persensitivity reaction, such as asthma, allergic rhinitis, atopic dermatitis, severe food allergies, chronic urticaria, angloedema or anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis, crype-I diabetes mellitus, or multiple sclerosis, and for preventing of, or symptoms resulting from, a type I hypersensitivity reaction in a subject receiving immunotherapy. The present sequence is the human IgE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 GGGGSFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA
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                                                                                    New fusion molecules comprising polypeptide sequences that bind to inhibitory receptor and native IgE receptor, useful for treating I mediated hypersensitivity reactions, e.g. asthma or allergies, or autoimmune diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ICRAVHEAASPSQTVQRAVSVNPGK 569
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IgE; allergy; human; antiallergic; immunosuppressive; antianaphylactic; antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IgE; vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
164 STTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSR
                                                                                                                                                        284 LPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL
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                                                                     PSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "Linker between domains C3 andC4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "IgE heavy chain C3 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "IgE heavy chain C4 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Epitope in BC loop"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Epitope in FG loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human IgE heavy chain C1-C2-C3-C4 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= IgE heavy chain
                                                                                                                                                                                                                                                                                                                                                 428
                                                                                                                                                                                                                                                                                                        569
                                                                                                                                                                                                                                                                                                                               404 ICRAVHEAASPSQTVQRAVSVNPGK
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15-SEP-2000; 2000US-0232831P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an immunoadhesin comprising: (a) a chimeric intercellular adhesion molecule (ICAM)-1 comprising a rhinovirus receptor protein linked to at least a portion of an immunoglobulin heavy chain; and (b) optionally a J chain and secretory component associated with the chimeric ICAM-1 molecule. The immunoadhesin has plant-specific of glycosylation and virucide activity. The immunoadhesin is useful for reducing infection by human rhinovirus (HRV) and hence the initiation or spread of the common cold by HRV. The immunoadhesin binds to HRV and reduces its infectivity, competing with cell surface ICAM-1 for binding creduces its infectivity, competing with cell surface ICAM-1 for binding creduces its infectivity, competing with cell surface ICAM-1 for binding creduces its infectivity in the immunoadhesin bin plants would be tetrameric, rather than dimeric.

Telease of viral RNA and formation of empty capsids. Expression of the immunoadhesin having multiple binding sites have a higher effective affinity for the virus, thereby increasing the effectiveness of the immunoadhesin. Association of secretory component and immunoglobulin J chain increases the stability of the immunoadhesin in the mucosal convironment. Production is significantly less expensive in plants than in animal cell culture and production in plants is safer for human use, since plants are not known to harbor any animal viruses. The present convirunce is that of a human immunoglobulin protein sequence, useful to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STIQEGELASIQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSR 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoadhesin for treating human rhinovirus infection comprises chimeric intercellular adhesion molecule-1, and optionally a J chain and secretory
                                                                                Human, immunoadhesin, intercellular adhesion molecule, ICAM-1,
human rhinovirus, immunoglobulin heavy chain, J chain, HRV, common cold,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --SRDFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA
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                                        Human Ig-E heavy chain constant region amino acid sequence.
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                                                                                                                                                                                                                                                                                                                                                                                            (PLAN-) PLANET BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                        28-APR-2001; 2001WO-US013932
                                                                                                                                                                                                                                                                                                                                                 28-APR-2000; 2000US-0200298P
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Larrick JW, Wycoff KL;
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N-PSDB; ABA05278.
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Best Local Similarity
                                                                                                                                transgenic plant
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                                                                                                                                                                        Homo sapiens
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This invention relates to a novel method for inducing an immune response against autologous immunoglobulin E (IgE) in an animal. The method comprises effecting simultaneous presentation of cytotoxic T lymphocyte (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell epitope (TH epitope) which is foreign to the animal, by antigen presenting cells (APCs) of the animal's immune system. The epitopes of the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autologous IgE in an animal, which is useful for downregulating autologous IgE in the animal. This method is useful in the prevention and treatment of allergic diseases such as anaphylaxis, allergic thinitis, asthma and atopic dermatitis. The present sequence represents the human IgE heavy chain C1-C2-C3-C4 domains used to create the epitopes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           364
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                                                           Inducing immune response against autologous immunoglobulin E in an animal, by effecting simultaneous presentation of cytotoxic T lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --SRDFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.7%; Score 1766; DB 5; Length 428; 78.0%; Pred. No. 1.6e-113;
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Gautam
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  428
Voldborg B,
                                                                                                                                 Example; Page 101-103; 151pp; English
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 Von Hoegen P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 347; Conservative
                               WPI; 2002-383033/41.
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The present sequence is that of the human IgE epsilon chain constant cregion. The invention is based on the discovery that a polypeptide that includes the CH1 (i.e. constant domain 1 in the heavy chain) and/or CH4 comain(s) of an IgE molecule, coupled to a carrier can be used to induce in a mammal. Compositions are provided for inducing self-specific anti-IgE catiobdies. These containing fragments of the immunised mammal. Compositions are provided for inducing self-specific anti-IgE coupled to polypeptides containing fragments of the IgE molecule, coupled to polypeptides containing fragments of the IgE molecule, coppied to polypeptides containing tragments of the IgE molecule, coppied to 105, 5-105 or 5-95 of the present sequence, while CH3 domain, but not the CH3 domain. CH1 polypeptides have at least 95% identity to amino acids 11-42% or 317-42% of the present sequence. The anti-IgE antibodies containinate the pool of free IgE in the mammal's serum. Alternatively, a polymuclectide encoding a fusion protein compositions and carrier and IgE-derived polypeptide is administered The compositions and carrier and IgE-derived polypeptide is administered The compositions and search to an allergic chintitis or conjunctivitis, an allergic reaction to an allergic full claimed)

C scema or urticaria (all claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -- 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Composition for treating immunoglobulin (Ig) E-mediated disorder such as anaphylactic shock, allergic rhinitis and conjunctivitis, comprises a polypeptide that includes CH1 and/or CH4 domains of IgE molecule coupled
                      urticaria; anaphylactic shock; allergic rhinitis; conjunctivitis;
antianaphylactic; immunosuppressive; antiallergic; antiasthmatic;
antiinflammatory; dermatological; vasotropic; ophthalmological; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 REPOVYTLPPSRDELTKNOVSLT--CLVKGFYPSDIAVEWESNGOPENNYKTTP-PVLDS
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               immunoglobulin E; antibody; human; allergy; asthma;
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Pred. No. 1.6e-113;
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                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                           (CYTO-) CYTOS BIOTECHNOLOGY AG.
(BACH/) BACHMANN M F.
(RENN/) RENNER W A.
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78.08;
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                                                                                                                                                                                                                                                                                                                                           27-JUL-2001; 2001WO-IB001353
                                                                                                                                                                           1. .110
/label= CH1
313. .428
/label= CH4
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                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                     ACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEF 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Producing cytotoxic T lymphocytes for treating e.g. autoimmune diseases, comprises culturing CD8+ T cells with antigen presenting cells to activate precursor CD8+ T cells specific for T the cell epitopes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytotoxic T lymphocyte; CTL; tumour; antigen presenting cell; allergy; lupus; autoimmune dieease; rheumatoid arthritis; autoimmune nephritis; psoriasis; APC; multiple sclerosis; autoimmune thyroiditis; hay fever; inflammatory bowel disease; insulin dependent diabetes; cell therapy; Crohn's disease; allergic rhinitis; graft versus host disease; asthma;
                                                                                                                            PSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTST
                                                                                                                                                                              GGGGSFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA
                      --SRDFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA
                                                    STTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQCHTFEDSTKKCADSNPRGVSAYLSR
                                                                                                                                                               LPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL
                                                                              STTÓEGELASTÓSELTLSOKHWLSDRTYTCOVTYOGHTFEDSTKKCADSNPRGVSAYLSR
                                                                                                           PSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunoglobulin E (IgE)
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                                                                                                                                                                                                                                                                                                                                                62
graft versus host disease and transplant rejection and/or allergic disease such as food allergy, hay fever, allergic rhinitis, allergic asthma and venom allergy. The invention is also useful in cell therapy. The present sequence is human immunoglobulin E (IGE) constant region. This protein is used in the exemplification of the invention. Note: This sequence is stated to be the same as that shown in figure 10 (AAB35114) of the specification. However these sequences differ
                                                                                                                                                                                                                                                                                                        129 REPOVYTLPPSRDELTKNOVSLT--CLVKGFYPSDIAVEWESNGOPENNYKTTP-PVLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164 STTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            224 PSPFDLFIRKSPITICLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              284 LPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                344 ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEF
                                                                                                                                                                                                                                                                                                                                186 VGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY-QQRSLSLSPGKVEGGGGSGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        485 ACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEF
                                                                                                                                                                                                                                                                                                                                                                                                                           63 SGHYATISLLTV-SGAWAK-QMFTCRVAHTPSSTDWVDNKTFSVC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STIQEGELASIQSELILSQKHWLSDRIYICQVIYQGHIFEDSTKKCADSNPRGVSAYLSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 GGGGSFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; pain; neuronal tissue; gene therapy;
spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                           24;
                                                                                                                                                                                                                     Length 428;
                                                                                                                                                                                                                   57.7%; Score 1766; DB 6;
78.0%; Pred. No. 1.6e-113;
iive 17; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Protein AAB59424, SEQ ID NO 14141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              404 ICRAVHEAASPSQTVQRAVSVNPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            545 ICRAVHEAASPSQTVQRAVSVNPGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADD48440 standard; protein; 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-2001; 2001US-0312147P, 01-NOV-2001; 2001US-0346382P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-AUG-2002; 2002WO-US025765
                                                                                                                                                                                                                                   Best Local Similarity 78.0%
Matches 347; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
                                                                                                                                                                             Sequence 428 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003016475-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-DEC-2004
29-JAN-2004
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                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
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ADE97382;
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                                                                                                                                                                                                   RESULT 12
                                                                                                                                                                                                                             ADE97382
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                               a
                                                                                                                               셤
                                                                                    ò
                                                                                                                                                                                                                                                                                                                                  The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal cubjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound which regulates the compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound to small molecule that regulates the activity of one or more of the polypeptides or their animal of one or more of the polypeptides or their animal of one or more of the polypeptides or their animal of one or more of the polypeptides or their anipodies. The polynucleotide or the compound that confication and a pharmaceutical composition comprising the one or more of molypeptides its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene for therapy). The sequence presented is a human protein (described in Table 3 therapy). The sequence presented is a human protein (described in Table 3 therapy). The sequence presented is a human protein (described in Table 3 therapy). The sequence presented is a human protein (described in Table 3 therapy). The sequence presented is a human protein (described in Table 5 therapy) is described by the sequence data for this patent did not form date of the print of the sequence data for his patent did not form date of the print of the sequence data for hi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 REPQVYTLPPSRDELTKNQVSLT.--CLVKGFYPSDIAVEWESNGQPENNYKTTP-PVLDS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 VGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY-QQRSLSLSPGKVEGGGGGGGGGG 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 QSPSVFPLTRCCKNIPSNATSVTLGCLATGYFPEPVWVTWDT-GSLNGTTMTLPATTLTL 62
                                                                                                                                                                                                                             New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSR
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57.7%; Score 1766; DB 7; Length 428;
Best Local Similarity 78.0%; Pred. No. 1.6e-113;
Matches 347; Conservative 17; Mismatches 57; Indels 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 SGHYATISLLTV-SGAWAK-QMFTCRVAHTPSSTDWVDNKTFSVC---
                                                                                                                 Costigan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                     Example 1; Page; 1017pp; English.
                                                                                                                 Befort K,
26-NOV-2001; 2001US-0333347P.
                                           (GEHO ) GEN HOSPITAL CORP. (FARB ) BAYER AG.
                                                                                                                                                            WPI; 2003-268312/26.
GENBANK; AAB59424.
                                                                                                                 D'urso D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 428 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         305
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129 REPQVYTLPPSRDELTKNQVSLT--CLVKGFYPSDIAVEWESNGOPENNYKTTP-PVLDS 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 VGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY-QQRSLSLSPGKVEGGGGSGGGGS 244
                                                              403
544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel immunoadhesin comprising a chimeric toxin receptor protein consisting of a toxin receptor protein linked to at least a portion of an immunoglobulin heavy chain with a J (joining) chain and secretory component (SC) associated with the chimeric toxin receptor protein. The immunoadhesin comprises a chimeric bacterial or viral toxin receptor protein and the immunoadhesin comprises a plant-specific glycosylation. The immunoadhesin of the invention demonstrates virucide and antibacterial activities and may be useful for reducing the binding of a viral or bacterial antigen to a host cell and thus for treating or preventing anthrax, as well as human rhinovirus infection which results in the common cold. The current sequence is that of the human immunoadhesion-related protein of the invention.
                                      485 ACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLBVTRAEWEQKDEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunoadhesin; immunoglobulin heavy chain; J chain; joining; toxin; virucide; antibacterial; anthrax; rhinovirus infection; common cold; intercellular adhesion molecule; ICAM-1; human; constant region; IgB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human IgE heavy chain constant region protein - SEQ ID 60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indela
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; Pred. No. 1.6e-113;
17; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 60; 288pp; English.
                                                                                                                                                                              Ŕ
                                                                                                                                       545 ICRAVHEAASPSQTVQRAVSVNPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PLAN-) PLANET BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                             ADE97382 standard; protein; 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.7%;
78.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-OCT-2002; 2002WO-US034197.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-OCT-2001; 2001US-00047542.
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Best Local Similarity 78.0%
Matches 347; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-FEB-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Larrick JW, Wycoff KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LARRICK J W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-636816/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (WYCO/) WYCOFF K L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ADE97381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003064992-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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us-09-847-208b-7.rag

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Gaps

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Length 493; Indels 296 220 356 280 416 340 476 400 536 460

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120 TISKAKVOPREPOVYTLPPSRDELTKNOVSLT--CLVKGFYPSDIAVEWESNGOPENNYK 177
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                                                                                                                                                                                                                                                                                                                    168 -----SVCSRDFTPPTVKILQSSCDGGHFPPTIQLLCLVSGYTPGTINITWLEDGQV
                                                                                                                                                                                                                                                                                                                                                                                                                      221 MDVDLSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TVSSASTQ--SPSVFPLTRCCKNIPSNATSVTLGCLATGYFPEPVMVTWDT-GSLNGTTM
                                                                                                                                                                                              TTP-PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGKVEGG
                                                                                                                                                                                                                            297 MDVDLSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               341 GTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human IgE heavy chain C1-C2-C3-C4 domains with MIGIS fragment.
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. 5e-113;
66;
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       DB 1;
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  Query Match
Best Local Similarity 77.0
Matches 349; Conservative
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transformed with recombinant DNA.
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12-FEB-1992
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/note= "Epitope in 301. .311

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Sequence 493 AA;

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This invention relates to a novel method for inducing an immune response against autologous immunoglobulin E (IgE) in an animal. The method comprises effecting simultaneous presentation of cytotoxic T lymphocyte (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell epitope (TH epitope) which is foreign to the animal, by antigen presenting cells (APCs) of the animal's immune system. The epitopes of the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autologous IgE in an animal, which is useful for downregulating autologous IgE in the animal. This method is useful in the prevention and treatment of allergic diseases such as anaphylaxis, allergic rhinitis, asthma and atopic dermatitis. The present sequence represents the human IgE heavy chain C1-C2-C3-C4 domains fused to the MIGIS fragment used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244
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                                                                                                                                                                                                                                                                                                                                                                                             Inducing immune response against autologous immunoglobulin E in an animal, by effecting simultaneous presentation of cytotoxic T lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin.
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                                                              C3 andC4"
                               "Epitope including C3C4 linker"
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                                                                                                                                                                                                                                                                                                                                  Gautam A;
                                                              'note= "Linker between domains
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e= "IgE heavy chain C4
"Epitope in FG loop'
                                                                                                                                                                                                                                                                                                                                  Voldborg B,
                                                                                                                           /note= "MIGIS fragment"
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2000US-0232831P
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/note= "F-
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Best Local Similarity
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15-SEP-2000;
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Matches
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The invention describes an isolated target immunoglobulin (Ig) derived protein comprising a target binding sequence and a portion of a heavy or light chain variable region and optionally a substitution, insertion or deletion as given in the specification. An isolated target Ig derived protein control of a heavy or light chain variable region comprising 10-125 or 10-75 contiguous amino acids chain variable region comprising 10-125 or 10-75 contiguous amino acids of the sequence comprising 10-138 or 77-107 amino acids, respectively, or its FR1, FR2, FR3 or FR4 fragment, or a portion of a heavy or light chain comprising 326-497 or 107 amino acids, respectively, or its FR1, FR3, FR4, CH1, CH2, CH3, hingel, hinge2, hinge3 or hinge4 fragment comprising 326-497 or 107 amino acids, respectively, or its FR1, FR2, FR3, FR4, CH1, CH2, CH3, hinge1, hinge2, hinge3 or hinge4 fragment composition. Also described are: an isolated nucleic acid encoding an isolated target Ig derived protein, a vector comprising the isolated conclaic acid; a prokaryotic or eukaryotic host cell comprising the isolated conclain and a carrier or diluent; an anti-idiotype Ig derived protein and a carrier or diluent; an anti-idiotype Ig derived protein comprising a target Ig derived protein, a method for that specifically binds target Ig derived protein; a method for corpan or animal, a medical device comprising the target Ig derived protein, an article of manufacture for human pharmaceutical or diagnostic use, comprising material and a container comprising a solution use, cumprising packaging material and a container comprising a solution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New target Ig derived protein comprising a target binding sequence and a portion of a heavy or light chain variable or constant region, useful in preparing a composition for diagnosing or treating a target related condition, e.g. tumor.
544
                                                                                         403
                                                                            ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEF
                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic, gene therapy; antibody; heavy chain variable region; diagnosis; pharmaceutical; tumor; cytostatic; neoplasm; IgE.
                                                                                                                                                                                                                                                                                                                                                                               Human variable heavy chain region IgE version 2.
                                                                                                                                  567
                                                                                                                                                                      426
                                                                                                                                                                                                                                                                    Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 35; 321pp; English.
                                                                                                                                                          | CRAVHEAASPSQTVQRAVSVNP
                                                                                                                                  ICRAVHEAASPSQTVQRAVSVNP
                                                                                                                                                                                                                                                                    ADW24784 standard; protein; 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-2003; 2003US-0483654P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUN-2004; 2004WO-US019783.
                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CENZ ) CENTOCOR INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2005-092074/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2005005604-A2
                                                                                                                                                                                                                                                                                                                                            07-APR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens
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--SRDFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSR 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RTLACLIQNEMPEDISVQMLHNEVQLPDARHSTTQPRXTKGSGFFVFSRLEVTRAEWEQK 541
                                                                                                                                                                                                                                                                                                                      244
                                                                                                                                                                                                                                                                                                                                                                                       245 GGGGSFTPPTVKILQSSCDGGGHPPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSR 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or lyophilized form of target Ig derived protein, and a method for producing an isolated mammalian target Ig derived protein. The target Ig derived protein is useful in preparing a composition for diagnosing or treating a target related condition in a cell, tissue, organ or animal, e.g. tumor. This is the amino acid sequence of variable heavy chain Negoin IgE. Note: This sequence differs from the version given in SEQ ID NO 35 in which the X residues have not been expanded to represent the whole CDR regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTST 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTS---GPRAAPEVYAFATPEWPGSRDK 481
                                                                                                                                                                                                                                                                                      62
                                                                                                                                                                                                                                                                        4 QSPSVFPLTRCCKNIPSNATSVTLGCLATGYPPEPVMVTWDT-GSLNGTTWTLPATTLTL
                                                                                                                                                                                                                                                                                                                                              PSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLIVTST
                                                                                                                                                                                                                                                     129 REPQVYTLPPSRDELTKNOVSLT--CLVKGFYPSDIAVEWESNGQPENNYKTTP-PVLDS
                                                                                                                                                                                                                                                                                                                      186 VGSFFLYSKLTVDKSRWQQGNVFSCSVMHBALHNHY-QQRSLSLSPGKVEGGGGSGGGG
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                    27;
                                                                                                                                                                                       Length 497;
                                                                                                                                                                                    57.3%; Score 1754.5; DB 9; Length 77.5%; Pred. No. 1.2e-112; Live 17; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFICRAVHEAASPSQTVQRAVSVNPGK 569
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Best Local Similarity 77.5'
Matches 347; Conservative
                                                                                                                                                       Sequence 497 AA;
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Search completed: November 30, 2005, 00:28:31 Job time : 192 secs

Thu Dec

GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd. Copyright

sw model using protein search, OM protein Run on:

November 30, 2005, 00:16:42; Search time 42 Seconds (without alignments) 1303.508 Million cell updates/sec

US-09-847-208B-7 3060 I EPKSCDKTHTCPPCPAPELL......HEAASPSQTVQRAVSVNPGK score: Title: Perfect

569

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched: 283416 of hits satisfying chosen parameters: Total number

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100 Listing first 45

pirl:* pir2:* pir3:* pir4:* PIR_80:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		epstron	epsilon-	gamma-	heavy ch	Ig gamma-1 chain C	gamma ch	gamma-3	gamma-3 chain	gamma-3 heavy	gamma-2	gamma-4 chain	gamma cha	gamma 2b	gamma 2a	gamma 4	epsilon	gamma-2 chain	gamma 1 chain	gamma 3	ש	g heavy ch	д датта-2b	g gamma-	g heavy ch	g gamma-1	gamma-3	010	_	Ig gamma-1 chain C
D		EHHO	I36948	GHHO	869339	S31866	PT0207	A23511	A60764	G3HUMI	G2HU	G4HU	GHRB	147160	147159	147162	EHRT	G2GP	147158	147161	S38864	S22080	PS0018	G3MSC	C30554	S31459	G3MSM	PC4436	GIMS	PS0017
DB	į į,	-	~	-4	7	4	~	~	7	ч	٦	Н	-	~	N	~	Н	Н	~	0	7	7	~	-	~	~	Н	~	Н	7
Lenath		428	426	330	374	255	234	377	377	289	326	327	323	328	328	277	429	329	328	328	548	470	333	329	308	472	398	444	324	326
% Query Match			55.7	40.0	•	6.	38.3	37.2	37.1	36.7	36.2	35.8	28.9	28.4	28.4	28.3	28.2	28.0	27.7	27.5		26.8	26.6	è.	9	è.	26.2	ý.	5.	25.6
ر د د		1766	1705.5	1225	1219	1217	1172	1138	1136	1123	1107	1097	883	868.5	868.5	865	862.5	858	847.5	40.	834.5	820	813	812.5	Ξ.	•			789.5	784.5
Result		-	8	m	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24		26			29

Ig gamma-1 chain C	Ig gamma-zc chain	Ig gamma-za chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig epsilon chain C	Ig gamma-2a chain	Ig gamma-2b chain	Ig epsilon chain C	Ig gamma-2a chain	Ig gamma-2b chain	Ig gamma-2 chain C	Ig gamma-2b chain	Ig gamma heavy cha	Ig epsilon chain C
GIMSM	S00847	G2MSA	537483	G2MSAB	GZMSAM	EHWS	S40295	G2MS11	EHMSS	PS0019	G2MSBM	806611	S01321	146732	PH1215
-	~	Н	N	-	m	-	~	-	Н	7	Н	~	~	7	7
393	329	330	469	335	399	388	446	474	423	322	405	327	475	180	227
25.6	25.4	25.4	25.4	25.2	25.2	25.0	24.9	24.6	24.5	24.4	24.4	24.0	23.9	21.9	18.8
784.5	776.5	176	176	772	771	766.5	761	751.5	750	747.5	746.5	735	731.5	699	576
30	31	32	33	3.4	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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RESULT 1
```

Gepsilon chain C region - human (Species: Homo sapiens (man) (Species: Homo sapiens (man) (Species: Homo sapiens (man) (Species: Janar-1981 #sequence revision 13-Jun-1983 #text change 09-Jul-2004 (Spacession: A2771; A23195; PH1214; A93491; A90824; A94418; B93933; S02438; A53116; C46 (Spacession: A2771; A23195; PH1214; A90824; A94418; B93933; S02438; A53116; C46 (Application of the sequence of a human immunoglobulin epsilon heavy chain constant region gene A; Reference number: A22771; MUID:84236029; PMID:6234164

A;Accession: A22771
A;Roidcule type: DNA
A;Roidcule type: DNA
A;Roidcule type: DNA
A;Roidcule type: DNA
A;Roidcule type: NA
A;Cross-references: UNIPROT: P01854; UNIPARC: UPI000004BB48; GB:L00022; GB:U00227; GB:V00\$
B;Ucda, S.; Nakai, S.; Nishida, Y.; Hisajima, H.; Honjo, T.
BEMBO J. 1, 1539-1544, 1982
A;Title: Long terminal repeat-like elements flank a human immunoglobulin epsilon pseudog
A;Reference number: A23195; MUID:84207910; PMID:6327276
A;Residues: 2-428 <UED>
A;Residues: 2-428 <UED>
A;Residues: 2-428 <UED>
A;Cross-references: UNIPARC:UPI0000173783; GB:J00222; NID:g184755
A;Cross-references: UNIPARC:UPI0000173783; GB:J00222; NID:g184755
A;Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splicing
A;Reference number: PH1214; MUID:92308B39; PMID:1613458

A; Accession: PH1214

A; Wolecule type: DNA
My Residues: 320-428 <ZHA>
My Residues: 320-428 <ZHA>
A; Cross-references: UNIPARC: UPI000014452D; EMBL: X63693; GB: S38668; NID: G32987
A; Cross-references: UNIPARC: Upidu, H.; Sasada, R.; Igarashi, K.; Kikuchi, M.; Sugly R; Seno, M.; Kurokawa, T.; Ono, Y.; Onda, H.; Sasada, R.; Igarashi, K.; Kikuchi, M.; Sugly R; Seno, M.; Kurokawa, T.; Ono, Y.; Onda, H.; Sasada, R.; Igarashi, K.; Kikuchi, M.; Sugly R; Seno, M.; Igarashi, K.; Kikuchi, M.; Sugly R; Seno, M.; Sasada, R.; Igarashi, M.; Sugly R; Sasada, R; Sasada, R; Sasada, R; Sasada, M.; Sasada, M.;

A;Accession: A93491
A;Accession: A93491
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rossiues: 1-428 <-SEN>
A;Cross-references: UNIPARC:UPI000004BB48; GB:L00022; GB:J00227; GB:V00555; NID:G185035
B;Max, E.E.; Battey, J.; Ney, R.; Kirsch, I.R.; Leder, P.
A;Hitle: Duplication and deletion in the human immunoglobulin epsilon genes.
A;Title: Duplication and deletion in the human immunoglobulin epsilon genes.
A;Reference number: A90824; MUID:83001945; PMID:6288268

A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: 1-358, 'L', 360-428 <MAX> A; Cross-references: UNIPARC: UP10000173784; GB:J00222; NID:g184755 A; Note: this sequence difference may be due to polymorphism R; Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H. R; Mennich, H.H.; Johansson, S.G.O.; Von Concepts and Developments, Bach, M.K., ed., pp.1-1. A; Reference number: A94418 A; Accession: A94418

A, Molecule type: protein

7.

Gaps

24;

Length 428;

DB 1; 4.2e-102 244 105

62

304 163 364 223 424 283

484 343 544 403

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A;Cross-references: UNIPARC:UPI000011754A; GB:M15398; NID:g176797; PIDN:AAA35416.1; PID:g
C;Genetics:
                                                                                                                                                                      129 REPQVYTLPPSRDELTKNQVSLT--CLVKGFYPSDIAVEWESNGQPENNYKTTP-PVLDS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig epsilon-chain - chimpanzee (fragment)
C;Species: Pan troglodytes (chimpanzee)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 --SRDFT-PTVKVLQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 LPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    485 ACLIONFMPEDISVOWLHNEVOLPDARHSTTOPRKTKGSGFFVFSRLEVTRAEWEQKDEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 REPQVYTLPPSRDELTKNQVSLT--CLVKGFYPSDIAVEWESNGQPENNYKTTP-PVLDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         305 STTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;336-405/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 SGHYATISLLTV-SGAWAK-QMFTCRVAHTPSSTDWVDNKTFSVC---
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R;Sakoyama, Y.; Hong, K.
R;Sakoyama, Y.; Hong, K.
A;Title: Naclectide sequences of immunoglobulin epsilon
A;Reference number: 136948; MUID:87147196; PMID:3103123
A;Accession: 136948
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-426 <RES>
                                  57.7%; Score 1766; DB 78.0%; Pred. No. 4.2e-ive 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 569
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                               Query Match 57.7%;
Best Local Similarity 78.0%;
Matches 347; Conservative
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AlyTitle: Characterization of four novel epsilon chain mRNA and a comparative analysis of Article: Characterization of four novel public characterization of four novel public characterization of the compared with conceptual translation
A.Accession: C46336
A.Accession: C46336
A.Accession: A6536
A.Accession: Ball mycloma U-266
A.Accession: Brelimiary
A.Accession: Brelimiary
A.Accession: A6536
A
A; Residues: 'GAWTL', 6,'X', 8-16,'B', 18-43,'B',45-52,55-92,95-97,'B',99-121,'B',123,'L',12
A; Crose_references: UNIPARC:UPID100017385
A; Experimental source: myeloma protein Nd
R; Kenten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.; G
R; Kenten, J.H.; Molgaard, Sci. US.A. 79, 6661-6665, 1982
A; Title: Cloning and sequence determination of the gene for the human immunoglobulin eps
A; Reference number: A93933; MUID:83065234; PMID:6815656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A. Modecule type: mRNA
A.Residues: 98-352 <IKE>
A.Cross-references: UNDARC:UPI0000173788
A.Stang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.
J. Biol. Chem. 269, 456-462, 1994
A.Fitle: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces
A.Reference number: A5316; MUID:94103254; PMID:8276835
                                                                                                                                                                                                                                                                                                                                                                                                                               of a recombinant human IgE Fc-epsilon fragmen
PMID:3121387
                                                                                                                                                                                                                                                                                                                                     UNIPARC:UPI0000173786; UNIPARC:UPI0000173787
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A;Residues: 320-428 <ZH2>
A;Cross-references: UNIPARC:UPI000014452D
A;Experimental source: myeloma U266-derived cell line AF-10
A;Note: sequence extracted from NCBI backbone (NCBIN:141701, NCBIP:141702)
R;Hellman, L.
                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-40;68-114;427-428 <KEN>
A;Cross-references: UNIPARC:UPI00001592FD;
                                                                                                                                                                                                                                                                                                                                                                 Rikeyama, S.
FEBS Lett. 224, 306-310, 1987
A;Title: Purification and characterization
A;Reference number: $02438; WUID:88083554;
A;Accession: $02438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: nucleic acid sequence not shown
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genes of chimpanzee and orangutat

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Gaps

25;

185

61

244 104

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A; Molecule type: protein
A; Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 24\footnote{A; Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 24\footnote{A; Cross-references: UNIPARC: UP1000017378F
A; Note: this sequence has the Gim(17) and Gim(1) markers
R; Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A; Title: Die Primaerstruktur des Kristallisierbaren monoklonalen Immunglobulins IgG1 KOL'
A; Reference number: A91723; MUID: 98284994
A; Contents: myeloma protein KOL; disulfide bonds
A; Accession: A91723
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A; Molecule type: protein
A; Rosidues: 1-96, Kr., 98-197, D', 199-238, 'E', 240,'M', 242-266,'D', 268-271,'D', 273-330 < SCH
A; Cross-references: UNIPARC: UP10000173790
A; Note: this sequence has the Glm(3) and Glm(non-1) markers
B; Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A; Reference number: A90565; MUID: 71064027; PMID: 4923144
A; Contents: annotation; disulfide bonds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ribreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N. Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob's physiole cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID:77070267; PMID:1002129
A;Contents: annotation; disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kath hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology
                      ioppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
1,Title: Die Primaerstruktur eines monoklonalen 19G1-Immunglobulins (Myelomprotein Nie);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
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F;20-85/Domain: immunoglobulin homology cIM2>
F;24-310/Domain: immunoglobulin homology cIM2>
F;24-310/Domain: immunoglobulin homology cIM3>
F;24-310/Domain: immunoglobulin homology cIM3>
F;27-33,144-204,25-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbobydrate (Asn) (covalent) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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40.0%; Score 1225; DB 1; Length 330;
Best Local Similarity 97.0%; Pred. No. 9.6e-69;
Matches 225; Conservative 3; Mismatches 4; Indels
                                                                                                                          A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
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S69339
Ig heavy chain V region precursor - human
H.; Hilschmann, N.
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A,Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194,'N', 196-197,'D', 199-238,'E', 240,
A,Cross-references: UNIPARC.UPI000017378E
A,Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met
                                                                                                                                                                                                                                                                                                                                                           162 SATQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGGTFEDSTKKCADSNPRGVSAYLSR 221
                                                                                                                                                                             424
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                                    STIQEGELASIQSELILSQKHWLSDRIYICQVIYQGHTFEDSIKKCADSNPRGVSAYLSR
                                                                                                                                                                             PSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTST
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Iggamma-3 chain C region (allotype G3m(b)) - human
Iggamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Sate: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Accession: A23511
R;Huck, S.; Port, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: com A;Reference number: A23511; MUID:86148507; PMID:3081877
A;Accession: A23511; MUID:86148507; PMID:3081877
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A; Residues: 1-377 <HUC>
A; Cross-references: UNIPARC: UPI000004718F; GB: X03604; GB: M12958; NID: g33070; PIDN: CAA2726
C; Genetics:
A; Gene: GDB: IGHG3
A; Gene: GDB: IGHG3
A; Gene: GDB: Ighg32, 33-14432.33
A; Map position: 14q32.33-14q32.33
A; Mitrons: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C; Superfamily: immunoglobulin C region; immunoglobulin homology
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                                               121 ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                   gamma chain C region - chimpanzee
C; Species: Pan troglodytes (chimpanzee)
C; Species: Pan troglodytes (chimpanzee)
C; Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C; Accession: Pr0207
R; Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A; Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A; Reference number: Pr0207; MUID:91287716; PMID:2062315
A; Accession: Pr0207
A; Molecule type: mRNA
A; Residues: 1-234 «EHR»
A; Residues: 1-234 «EHR»
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: immunoglobulin
                                                                                                     144 ISKAKGOPREPOVYTLPPSRDELIKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 38.3%; Score 1172; DB 2; Best Local Similarity 95.6%; Pred. No. 1.2e-65; Matches 215; Conservative 4; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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S11866
Ig gamma-1 chain C region - synthetic
Ig gamma-1 chain C region - synthetic
() Species synthetic
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C;Accession: S31866
C;Accession: S31866
Synthy Data Library, February 1993
A;Description: Screeing method for protein-protein interactions of cloned gene products.
A;Reference number: S31866
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C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: 86939; 872664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Birchem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: 869339; MUID:95262687; PMID:7744049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N#YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 143
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A; Status: preliminary
A; Modeduel type: mRNA
A; Residues: 1-374 «KHA>
A; Cross references: UNIPARC: UPI0000176F24; EMBL: X81695
R; Khamlichi, A.A.
A; Accession: S72664
A; Reference number: S72664
A; Accession: S72664
A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 374;
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Pred. No. 2.6e-68;
5; Mismatches 4;
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Best Local Similarity 96.1%;
Matches 223; Conservative
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Best Local Similarity
Matches 224; Conserv
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A;Molecule type: mRNA
A;Residues: 1-255 <FIL>
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A, Cross-references: UNIPARC:UP10000173797
A, Cross-references: UNIPARC:UP10000173797
A, Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchaift, A, Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchaift, A, Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 co A, Note: the sequence of residues 42-76 was taken from the reference that follows
R; Michaelsen, T.E.; Frangione, B.; Franklin, E.C.
A, Biol. Chem. 252, 883-889, 1977
A, Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplicatioh A, Reference number: A92219; MUID:77118561; PMID:402363
A, Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Reaidues: 59-125, TBF, 128-226, 228-289 <WOL>
A;Cross-references: UNIPARC:UPI0000173799
A;Cross-references: UNIPARC:UPI0000173799
A;Cross-references: UNIPARC:UPI000173799
A;Cross-references: UNIPARC:UPI000173799
Broc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A;Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deletion A;Reference number: A93915; MUID:82247835; PMID:6808505
A;Contents: heavy chain disease protein Omm
A;Accession: A93915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 12-70;72-114;116-125, E',127-133, 'L',135-136,'E',138,'Y',140-154,'D',156-15<sup>†</sup>
A;Cross-references: UNIPARC:UPI000017379A; UNIPARC:UPI000017379B; UNIPARC:UPI000017379C)
A;Note: a carboxyl-terminal Lys is removed posttranslationally
A;Note: this sequence may represent an allelic form or another gamma chain subclass
                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPARC:UPI0000173798
A;Note: the hinge region in gamma-3 chains is about four times as long as in other gamm#idue segment (12-28)
                                                                                                                                                                                                                                                                                                                                                                                                                                            A)Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inter R; Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.
Blochem. Blophys. Res. Commun. 71, 907-914, 1976
A;Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the A;Reference number: A90198; MUID:77021516; PMID:823945
A;Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238
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A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin C region; immunoglobulin; pyroglutamic acid C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid F;2370/Domain: immunoglobulin homology <IMM>
F;17Modified site: pyrrolidone carboxylic acid (Gln) #status experimental F;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental
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88.3%; Pred. No. 1.7e-62;
iive 14; Mismatches 13;
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Best Local Similarity 88.3%,
Matches 204; Conservative
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G3HUM1

G3HUM1

G3HUM2

G3HUM2

L; ggamma-3 heavy chain disease proteins - human

C; Species: Homo sapiens (man)

C; Species: Homo sapiens (man)

C; Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999

C; Accession: A90442; A2219; Ā90198; A33915; A02149

R; Frangione, B: Rosenwasser, E: Frenlli, F:; Franklin, E.C.

Biochemistry 19, 4304-4308, 1980

A; Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-A; Reference number: A90442; MUID:81021548; PMID:6774747

A; Contents: heavy chain disease protein Wis

A; Molecule type: protein
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Ig gamma-3 chain C region, form LAT - human
C;Species: Homo sapiens (man)
C;Accession: A60764
R;Huck, S; Lefranc, G; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, bl, c3, c5, u) with an IGHG4
A;Reference number: A60764; MUID: 90007613; PMID: 2571587
A;Accession: A60764
A;Scatus: preliminary
A;Molecule type: DNA
A;Residues: 1-37 cHUC>
A;Residues: 1-37 cHUC>
A;Cross-references: UNIPROT: OBN4Y9; UNIPARC: UPI0000176F0B
C;Superfamily: immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>
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                                                                                                                        206 KWYVDGVEVHNAKTKPREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 265
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                                                                                                                                                                                                   61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
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.larity 89.7%; Pred. No. 3.7e-63;
Conservative 11; Mismatches 13; Indels (
                              Indels
2.8e-63;
                                 11; Mismatches
   Pred. No.
   89.78;
                                 208; Conservative
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A,Rolecule type: DNA
A,Residues: 1.327 (ELL)
A,Cross-references: UNIPROT:P01861; UNIPARC:UPI000047190
A;Note: the sequence was determined from the germine gene
A;Note: the sequence was determined from the granine gene
R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
R;Pink, J.T. 33-47, 1970
     36.2%; Score 1107; DB 1; 188.4%; Pred. No. 1.9e-61; ive 12; Mismatches 11;
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A;Map position: 14432.33-14432.33
A;Introns: 99/1; 111/1; 221/1
C;Complex: An imm...-
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DNA 1, 11-18, 1981
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Best Local Similarity 88.45
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Biochem. J. 121, 217-225, 1971

A; File: Disaulphide bridges of the heavy chain of human immunoglobulin G2.

A; Reference number: A90253; MUID:72033500; PMID:940472

A; Contents: annotation; myeloma protein Sa, disulfide bonds

R; Frangione, B.; Milstein, C.; Pink, J.R.L.

Nature 221, 145-148, 1969

A; Contents: annotation; Sa, disulfide bonds

C; Genetics:
A; Contents: annotation; Sa, disulfide bonds

C; Genetics:
A; Complex: A913-1493.33

A; Contents: annotation; Sa, disulfide bonds

C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin heterotetramer; immunoglobulin

C; Superfamily: immunoglobulin homology <IMI>
F; 133-202/Domain: immunoglobulin homology <IMI>
F; 133-202/Domain: immunoglobulin homology <IMI>
F; 134-202/Domain: immunoglobulin homology <IMI>
F; 134-202,Domain: immunoglobulin homology <IMI>
F; 135-3146-200, 246-304/Disulfide bonds: interchain (to heavy chain) #status experimental
F; 176/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A.Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and falserence number: A92809; MUID:81007873; PMID:6774012
A.Koctession: A92809
A.Molecule type: protein
A.Kecession: A92809
A.Molecule type: protein
A.Koctesion: A92809
A.Molecule type: protein
A.Koctesion: Dischem: A92809
A.Molecule type: protein
A.Koctes Trp-156 is at or near the complement-binding site
R.Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem: 57, 758-767, 1979
A.Title: The amino acid sequences of the three heavy chain constant region domains of a A.Title: The amino acid sequences of the three heavy chain constant region domains of A.Koctesion: A90752; MUID:80001357; PMID:113060
A.Contents: myeloma protein Zie
A.Molecule type: protein
A.Koctesion: A90752
A.Molecule type: protein
A.Keferences: UNIPARC:UPI0000173792; UNIPARC:UPI0000173793
A.Molecule type: Trotein
A.Keferences: UNIPARC:UPI0000173792; UNIPARC:UPI0000173793
A.Molecule type: Parr, D.M.
A.Consa.references: UNIPARC:UPI0000173792; UNIPARC:UPI0000173793
A.Molec: this sequence has since been revised
A.Keference number: A93132; MUID:80114419; PMID:118920
A.Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g.A.Reference number: A93132; MUID:80114419; PMID:118920
C; Species: Homo sapiens (man)
C; Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 09-Jul-2004
C; Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 09-Jul-2004
C; Date: 30-Apr-1981 #sequence possible pos
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A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidati
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A, Accession: A93132
A, Accession: A93132
A, Residues: Z38-275 < HOF>
A, Cross-references: UNIPARC:UPI0000173794
R, Hofmann, T.: Parr, D.W.
submitted to the Atlas, March 1980
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Biochem. J. 117, 33-47, 1970
A;Title: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant re
A;Reference number: A90249; MUID:70207560; PMID:4192699
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                                                                                                                                                                                                                                     155 NWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLFAPIEKT 214
                                                                                                                                                                                                                                                                                                                                                                              215 ISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70
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F:240-307/Domain: immunoglobulin homology <IM3>
F:240-307/Domain: immunoglobulin homology <IM3>
F:244/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,141-201,247-305/Disulfide bonds: #status predicted
F:20-8105/Disulfide bonds: interchain (to heavy chain) #status experimental
F:107/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig gamma-4 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C;Accession: A90933; A90249; Ā02150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                  1 BPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                     NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene
A,Reference number: A90933; MUID:83157104; PMID:6299662
4 ;
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Pred. No. 8e-61;
1; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Accession: A90249
A, Modecule type: protein
A, Residues: 1-30;81-326 < PIN>
A, Cross-references: UNIPARC: UPI0000173795; UNIPARC: UPI0000173796
Indels
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A; Cross-references: UNIPARC: UPI0000115525; EMBL: U03780; NID: 9433125; PIDN: AAA52218.1; P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47160
J: Immunol: 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47160
                                                                                                                                                                                                                         EWESNGOPENNYKTTPPVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQR 224
                                                                                                                                                                                                                                                105 KCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV 164
76 QPVTCNVAHPATNTKVDKTVAPSTCSKPTCPPPELLGGPSVFIFPPKPKDTLMISRTPEV 135
                                                                          TCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tch 28.4%; Score 868.5; DB 2; al Similarity 70.1%; Pred. No. 1.1e-46; 157; Conservative 32; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig gamma 2b chain constant region - pig (fragment)
                                                                                                                                                                                                                                                                                                                        225 SLSLSPGK 232
                                                                                                                                                                                                                                                                                                                                                                  SISRSPGK 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-328 < KAC>
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Best Local S
Matches 157
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147159
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A,Residues: 1-323 <BER>
A,Residues: 1-323 <BER>
A,Cross-references: UNIPROT:P01870; UNIPARC:UPI000012B37D
A,Cross-references: UNIPROT:P01870; UNIPARC:UPI00012B37D
A,Mole, Lister, D.M.; Mole, L.E.
Biochem. J. 151, 337-349, 1975
A,Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglob
A,Reference number: A90290; MUID:76135469; PMID:1243651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Modecule type: protein
A; Residues: 1-47, 'E', 49-71,' PV', 72-128 <PRA>
A; Residues: 1-47,' E', 49-71,' PV', 72-128 <PRA>
A; Cross-references: UNIPARC: UP100001737AB
Martens, C.L.; Moore, K.W.; Steinmeth, Hood, L.; Knight, K.L.
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
A; Title: Heavy chain genes of rabbit 1gG; isolation of a cDNA encoding gamma heavy chain
A; Reference number: A93928; MUID: 81299917; PMID: 6193512
                                                                                                                                                                                                                                                                                 Ig gamma chain C region - rabbit (c)species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 24-Apr-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jul-2004
C;Accession: A91749; A90290; A93328; A90245; A94416; A02161
R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
A;Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplot A;Reference number: A91749; MUID:84030930; PMID:6313520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                  PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFF 190
                                                            226 PQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F:130-199/Domain: immunoglobulin homology <1M2>
F:236-303/Domain: immunoglobulin homology <1M3>
F:173/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 28.9%; Score 883; DB 1; Length 323; Best Local Similarity 64.5%; Pred. No. 1.4e-47; Matches 160; Conservative 34; Mismatches 38; Indels
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gramma 2a chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: 21-86-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147159
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Reference number: 147159; MUID:95015845; PMID:7930579
A;Accession: 147159
                                               7
                                                                                                                                                                                                                                                                                                                                                      284
                                                                                                                          71 NVKTKPREEQYNSTYRVVSVLTVLHQNWMNCKEYKCKVSNKALPAPIEKTISKAKVQPRE 130
                                                                                                                                                                                                                           165 TAQTRPKEEQFNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTRE 224
                                                                                                                                                                                                                                                                                                  131 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSVGS 188
                                                                                                2
                                                                                                                                                                                                                                                                                                                              11 CPPCPAPELLGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
                                               Gaps
                                               3;
Length 328;
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                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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--TC--PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV

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RESULT 15
147162
1g gamma 4 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147162
R;Accession: 147162
A;Title: Five putative subclasses of swine 1gG identified from the cDNA sequences of a A;Title: Five putative subclasses of swine 1gG identified from the cDNA sequences A;Accession: 147163
A;Accession: 147163
A;Accession: 147164
A;Residues: 1-277 <KAC>
A;Cossion: 147165
A;Cossion: 147165
A;Cossion: 147165
A;Cossion: 147165
A;Cossion: 147165
A;Cossion: 14716
A;Cossion: 1471
                                          PI
                                 A;Cross-references: UNIPARC:UPI000115524; EMBL:U03779; NID:g433123; PIDN:AAA52217.1; C;Genetics:
A;Gene: IgG2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 GVEVHTAQTRPKEEQFNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAK 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169 GQTREPQVYTLPPPTEELSRSKVTLTCLVTGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQ 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 CPICPACE-SPGPSVFIFPPFKPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVH 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 NVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPRE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 TAQTRPKEEQFNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGGTRE 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSVGS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225 PQVYTLPPHAGELSRSKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGT 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 GVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 VQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 70
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                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 28.3%; Score 865; DB 2; Length 277; Il Similarity 69.0%; Pred. No. 1.5e-46; Conservative 32; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        285 YFLYSKFSVDKASWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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ne : 43 secs
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Best Local Similarity
Matches 158; Conserva
A; Residues: 1-328 < KAC>
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PRELIMINARY PROTEIN SEQUENCE (MYELOMA PROTEIN ND).
Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
(In) Bach M.K. (eds.);
Immediate hypersensitivity: modern concepts and developments, pp.1-36,
Marcel Dekker, New York (1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-83065234; PubMed-6815656;
Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney
Bell L.O., Gould H.J.;
"Cloning and sequence determination of the gene for the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE OF 1-40; 68-114 AND 427-428
                                                                                                                                                                                    Homo sapiens (Human)
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MEDIINE-83001945; PubMed-6288268; DOI=10.1016/0092-8674(82)90185-4;
MAX E.E., Battey J., Ney R., Kirsch I.R., Leder P.;
"Duplication and deletion in the human immunoglobulin epsilon genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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MEDLINE=83168897; PubMed=6300763;
Seno M., Kurokawa T., Ono Y., Onda H., Sasada R., Igarashi K.,
Kikuchi M., Sugino Y., Nishida Y., Honjo T.;
"Molecular cloning and nucleotide sequencing of human immunoglobulin
epsilon chain cDNA.";
Nucleic Acids Res. 11:719-726 (1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=84236029; PubMed=6234164;
Flanagan J.G., Rabbitts T.H.;
"The sequence of a human immunoglobulin epsilon heavy chain constant
region gene, and evidence for three non-allelic genes.";
EMBO J. 1:655-660(1982).
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MEDLINE=84207911; PubMed=6127276;
MEDLINE=84207911; PubMed=6127276;
Uloda S., Nakai S., Nishida Y., Hisajima H., Honjo T.;
"Long terminal repeat-like elements flank a human immunoglobulin epsilon pseudogene that lacks introns.";
EMBO J. 1:1539-1544(1982).
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Ig epsilon chain C region.
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                                                                 Q6MZU6_HUMAN
Q6P6C4_HUMAN
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Q8TC63_HUMAN
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     IGHG3 HUMAN
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                                                                                              This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                           MEDLINE=87089848; PubMed=3796618; DOI=10.1016/0161-5890(86)90005-2; Padlan E.A., Davies D.R.; Padlan E.A., Davies D.R.; Model of the Fc of immunoglobulin E."; Mol. Immunol. 23:1063-1075(1986).
-!- SIMILARITY: Contains 4 Ig-like (immunoglobulin-like) domains.
immunoglobulin epsilon chain expressed in a myeloma cell line.";
Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
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/FTId=VAR_003885.
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PIR, A22771; BHHU.

PUB; 1FP6; X.ray; B/D=211-428.

PDB; 1G84; NVR; A=106-208.

PDB; 1G84; NVR; A=106-208.

PDB; 1G84; NVR; A=106-208.

PDB; 1G84; NVR; A=106-208.

PDB; 1G84; NVR; A=106-428.

PDB; 1G84; NVR; A=106-427.

Ensembl; ENSGO000177154; Howo sapiens.

HGWC; HGWC: 5222; IGHE.

MIGNC; HGWC: 5222; IGHE.

MIGNG; HGWC: 5222; IG
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47019 MW; 25C4CA072AA558A0 CRC64;
                                             57.7%; Score 1766; DB 1; 178.0%; Pred. No. 3.4e-111; 1ive 17; Mismatches 57;
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"Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus aureus at 2.9 - and 2.8 A resolution."; Biochemistry 20:2361-2370(1981).

-i- MISCELLANEOUS: Nie has the GIM(17) allotypic marker, 97-K, and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN SEQUENCE (MYELOMA PROTEIN NIE).

MEDLINE=77070269; PubMed=826475;
Ponsting1 H., Hilschmann N.;
Ponsting1 H., Hilschmann N.;
"The rule of antibody structure. The primary structure of a monoclonal 1gG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                              PROTEIN SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
MEDLINE=71064024; PubMed=5489771;
Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
Waxdal M.J., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. VII. Amino
acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
Biochemistry 9:3161-3170(1970).
                                                                                                                                                                                                                                                                                                                                                                                          "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7."; Biochemistry 9:3171-3181(1970).
                                                                                                                                                               MEDLINE-82274238; PubMed=6287432;
Ellison J.W., Berson B.J., Hood L.E.;
"The nucleotide sequence of a human immunoglobulin C gammal gene.";
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Dreker L., Schwarz J., Reichel W., Hilschmann N.;
Dreker L., Schwarz J., Reichel W., Hilschmann N.;
Rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie), I: purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-83289111; PubMed-6884994; Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.; Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."; Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
                                                                                                                                                                                                                                                                                                                                          PROTEIN SEQUENCE OF 136-129 (EU).
MEDLINE=71064025; PubMed=5530842;
Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE=71064027; PubMed=4923144;
Gall W.E., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. X.
Intrachain disulfide bonds.";
Biochemistry 9:3188-3196(1970).
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  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-MAY-2005 (Rel. 47, Last annotation update)
1g gamma-1 chain C region.
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MEDLINE=81208100; PubMed=7236608;
                                                                                                                                                                                                         Nucleic Acids Res. 10:4071-4079(1982).
                                                                      Homo sapiens (Human)
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GIM(1) markers, 239-D and 241-L. KOL and EU sequences have the GIM(3) marker and the GIM (non-1) markers.

-!- MISCELLANEOUS: Nie also differs in the amidation states of 35, 116, 198, 269 and 272.

-!- MISCELLANEOUS: EU also differs in the amidation states of residues 155, 166, 177, 195, 198, 269, and 272 and in the order of residues 268-272.
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/FIId=VAR_003887.
L -> M (in GlM(lnon-1) marker).
/FIId=VAR_003888.
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Interchain (with heavy chain)
Interchain (with heavy chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R PDB; 1D5B; X-ray; B/H=1-101.

R PDB; 1D5B; X-ray; B/H=1-101.

R PDB; 1D5B; X-ray; B/H=1-101.

R PDB; 1DNZ; X-ray; B/H=1-101.

R PDB; 1DNZ; X-ray; A/B=106-330.

R PDB; 1E4K; X-ray; A/B=106-329.

R PDB; 1ECZ; X-ray; A/B=106-329.

R PDB; 1FCZ; X-ray; A/B=106-329.

R PDB; 1FCZ; X-ray; A/B=107-330.

R PDB; 11CS; X-ray; A/B=107-330.

R PROSITE; PSO0290; 1G/PMC; 2.

R PROSITE; PSO0290; 1G/PMC; 3.

R PROSITE; PSO0290; 1G/PMC; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                     J00228; AAC82527.1; ALT_INIT; Genomic_DNA.
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                                                                                                                                                                                                              residues 198, 267 and 272.
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B/H=1-101.
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1D5B; X-ray; H
1D5D; X-ray; H
1D6V; X-ray; H
1DN2; X-ray; A
1B4K; X-ray; A
1FC1; X-ray; A
1FC2; X-ray; A
1FCC; X-ray; A
1HCC; X-ray; A
1HCC; X-ray; A
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REGION
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TISSUB-Primary B-Cells,

WEDLINE-2388257; PubMede-12477932; DOI=10.1073/pnas.242603899;

STRAUSPER R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,

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A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

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Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

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A Rodriquez A.C., Grimwood J., Schmutz J., Myers R.M.,

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Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield A.S., John J.E., Johns S.J.M., Marra M.A.;

"""" "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
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                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISKTPEVTCVVVDVSHEDPEVKF
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40.0%; Score 1225; DB 2; Length 465;
Best Local Similarity 97.0%; Pred. No. 1.6e-74;
Matches 225; Conservative 3; Mismatches 4; Indels
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; BCO7366; AAH73766.1; -; mRNA.
GO; GO:0016021; C:integral to membrane; IEA.
InterPro; IPR003159; Ig.
InterPro; IPR003109; Ig_C1.
InterPro; IPR003100; Ig_MRC.
InterPro; IPR00359; Ig_WC.
InterPro; IPR00359; Ig_WC.
InterPro; IPR00359; Ig_WC.
InterPro; IPR00359; Ig_WC.
InterPro; IPR00359; Ig_W.
SMART; SM00407; IGC1; 3.
SWART; SM00407; IGC1; 3.
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PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Hypothetical protein.
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TISSUE=Primary B-Cells;
 Hypothetical protein.
                  (Human)
                                                                                              NUCLEOTIDE SEQUENCE
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                                                                  NCBI_TaxID=9606;
                Homo sapiens
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Last annotation update)
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QGGMXG HUMAN
D QGGMXG HUMAN PRELIMINARY;
AC QGGMX6;
DT 05-UUL-2004 (TERMBLE): 27,
DT 05-UUL-2004 (TERMBLE): 27,
C DT 05-UUL-2004 (TERMBLE): 27,
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Matches 225; Conservative
330 AA;
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SEQUENCE
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MEDLINE-22380257; PubMed=12477932; DOI=10.1073/pnas.242603899;

NETAGUBERT R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altsubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.E., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Schalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 EPKSCDKTHTCPPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCWVDVSHEDPEVKF 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                          Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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40.0%; Score 1225; DB 2; Length 466;
Best Local Similarity 97.0%; Pred. No. 1.6e-74;
Matches 225; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Peripheral Nervous System;
NIH MCC Project;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC072419; AAH72419.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 2.
SEQUENCE 466 AA; 50854 MW; 53EBOBCEDE81076E CRC64;
                                                  Created)
Last sequence update)
Last annotation update)
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                   466 AA.
                 PRT;
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InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.
InterPro; IPR003597; Ig.
InterPro; IPR003597; Ig.
InterPro; IPR003596; Ig.
Pfam; PP07654; C1-8et; 3.
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                 QGIN78_HUMAN PRELIMINARY;
                                                                         05-JUL-2004 (TrEMBLrel. 05-JUL-2004 (TrEMBLrel.
                                                       05-JUL-2004 (TrEMBLrel.
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SMART; SM00407; IGc1; 3
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                               IGHG1 protein.
                                                                                                                                  Name=IGHG1
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A Strausberg K. D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D., Riqueberg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D., Riqueberg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scapleron M. S. Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., As Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C., Anha S.S., Loquellano N.M., Peters G.J., Maramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratene P.H., Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Yilalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Allalon D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A., Allakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Budfard G.G., Butteffield X.S.N., Krzywinski M.I., Skalake U., Smallus D.E., Schmerch A., Schein J.E., Jones S.J.M., Marra M.N., Schnert D.M., Schmert D.M., Marra M.N., Schnert D.M., Schmert D.M., Marra M.N., Schein J.E., Jones S.J.M., Marra M.N., Schnert D.M., Schein J.E., Jones S.J.M., Marra M.N., Schein J.E., Jones S.J.M., Marra M.N., Schnert D.M., Schein J.E., Jones S.J.M., Marra M.N., Schein J.E., J.M., Marra M.N., Schein J.E., J.M., Marra M.N., Schein J.E., Schein J.E., Schein J.E., Schein J.E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 158 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNQPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            469
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NIH MGC Project;
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BC092518; AAH99518.1; -; mRNA.
SROUENCE 469 AA; S1254 MW; AC13448E3047784F CRC64;
                                                                                                                                                                                                                                                               Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                        Last sequence update)
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ilarity 97.0%; Pred. No. 1.6e-74;
Conservative 3; Mismatches 4;
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                                                                                                                                                                                                               Created)
                                                                                                                                                                                                             10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30,
                                                                                                                                                                Q569F4 HUMAN PRELIMINARY;
Q569F4;
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                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                          IGHG1 protein.
Name=IGHG1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTYLHQDWLNGKEYKCKVSNKALPAPIEKT 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                           TISSUE=Spleen;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
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                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1225; DB 2;
Pred. No. 1.6e-74;
                          469 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                    Created)
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                        Q727P5_HUMAN PRELIMINARY;
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                                                                                    01-OCT-2003 (TrEMBLrel. 01-MAR-2004 (TrEMBLrel.
                                                              01-OCT-2003 (TrEMBLrel.
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SEQUENCE 469 AA; 5:
                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IISSUE=Spleen;
                                                                                                                                                       Name=IGHG1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238
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A Straubberg R.L., Feingold B.A., Grouse L.H., Derged J.G.,

A Straubberg R.L., Feingold B.A., Grouse L.H., Derged J.G.,

A Itschil S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Blate N.K.,

A Itschil S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Hishe F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.F.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosk S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Standard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia S., Sanchez A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Bring M., Madan A., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Bring M., Madan A., Schein J.E., Jones S.J.M., Marra M.A.;

Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Spleen;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
418 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSFGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 470;
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PROSITE; PS00290; IG_MHC; UNKXOWN 2.
Hypothetical protein; Immunoglobulin domain.
SEQUENCE 470 AA; 51204 MW; 7780F34521483E1A CRC64;
                                                                                                                                                                                                                                                                                     01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0RT-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
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Pred. No. 1.6e-74;
3; Mismatches 4;
                                                                                                                                                                                                                         AA.
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HSSP; P01857; 1HZH.
INTEAPTO; 1PR007110; 1g-like.
INTEAPTO; 1PR003597; 1g-c1.
INTEAPTO; 1PR003006; 1g-MHC.
INTEAPTO; 1PR003596; 1g-W.
PFam; PF07654; C1-set; 3.
SMART; SM00406; 1GV; 1.
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Best Local Similarity 97.0%;
Matches 225; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA sequences."
                                                                                                                                                                                                                     Q7Z5W1_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                               Q7Z5W1;
                                                                                                                                                  RESULT 7
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The German cDNA Consortium;
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QGN089;
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Matches 225; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             rissum=Rectum tumor;
                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
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            61
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NEULBOILE R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B.B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

NA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rachey J., Helton E., Ketreman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shewchenko Y., Bouffard G.G.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
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359 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 418
                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                         419 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSFGK 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Primary B-Cells;
NIH MGC Project;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO18747; AAH18747.1; -; mRNA.
HSSP; P01861; 1ADQ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                      470 AA
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PROSTIE; PS60290; IG MIC; UNKNOWN 2.
CENTRACE 470 AA; 51716 MW; 78495
                                                                                                                        PRT;
                                                                                                                                                   Created)
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InterPro; IPR003599; Ig.
InterPro; IPR00110; Ig-like.
InterPro; IPR003597; Ig-like.
InterPro; IPR003596; Ig-MC.
InterPro; IPR003596; Ig-W.
Ffam; PR07654; C1-8et; 3.
SMART; SM00409; IG; 2.
SMART; SM00400; IG; 3.
SMART; SM00400; IGC; 3.
                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                  QEPJA4_HUMAN PRELIMINARY;
QEPJA4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.
                                                                                                                                                                                                                  Homo sapiens (Human).
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                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                            IGHG1 protein.
                                                                                                                                                                                                           Name=IGHG1;
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NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                            ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.; Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases. EMBL; BX640627; CAE45781.1; -; mRNA. HSSP; P01861; IADQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PVLDSVGSFFLXSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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                                                                                                                                                                                         181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein. SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                              472 AA
                                                                                                                                                                                                                                                                                                                                                                                                        05-UUL-2004 (TrEMBLrel. 27, Created) 05-UUL-2004 (TrEMBLrel. 27, Last seq 05-UUL-2004 (TrEMBLrel. 27, Last and Hypothetical protein DKFZp686F15220. Name-DKFZp686F15220.
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PROSITE; PS00290; IG MHC; UNKNOWN 2.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_MHC.
Pfam; PF07654; C1-8et; 3.
SMART; SM00407; IGC1; 3.
SMART; SM00407; IGC1; 3.
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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Alausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A popking R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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A Hathon B., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
C. Generation and initial analysis of more than 15,000 full-length human
                 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                 sednences."
                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                               and mouse cDNA
                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   364 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                              Gaucher C., Klein P., Beliard R.,

Gaucher C., Klein P., Beliard R.,

"Sequence determination of the recombinant human anti-RhD monoclonal
antibody T125."

Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.

R EMBL, AY894992, AAW82028.1; -; mRNA.

InterPro: IPR007110; Ig-11.e.

R InterPro: IPR007110; Ig-11.e.

R InterPro: IPR003599; Ig-11.e.

R InterPro: IPR003596; Ig-NC.

R InterPro: IPR003596; Ig-NC.

R InterPro: IPR003596; Ig-NC.

R Pfam; PF07668; V-set; 1.

R SWART; SW00409; IG-1.3.

R SWART; SW00409; IG-1.3.

R RRART; SW00409; IG-1.4.

R PROSITE; PS00290; IG-IKE; 4.
                                                                                                                    Dukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 BPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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anti-RhD monoclonal T125 gammal heavy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                           10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Anti-RhD monoclonal T125 gammal heavy chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1367D400DC7D2859 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.0%; Score 1225; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.6e-74;
               475 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
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                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             475 AA; 52362 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, Hypotherical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.08;
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QEGMW7;
               QEFES_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 225; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19
                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                       NCBI_TaxID=9606;
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O6GMW7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                              Length 475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
Strausberg R.; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                              51987 MW; 2A1FE55D736860F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                           Score 1225; DB 2;
Pred. No. 1.6e-74;
3; Mismatches 4;
                                   EMBL; BC07782; AAH73782.1; -; mRNA.
GO; GO:0016021; C:integral to membrane; IEA.
InterPro; IPR003159; Ig.
InterPro; IPR003109; Ig.
InterPro; IPR003109; Ig.
InterPro; IPR00359; Ig.
InterPro; IPR00407; IGC1; 3.
SWART; SW004007; IGC1; 3.
                                                                                                                                                                                                                                                                                              PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Hypothetical protein_
SEQUENCE 475 AA; 51987 MW; 2A1FE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                40.0%;
97.0%;
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 97.01
Matches 225; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QEGMX1 HUMAN PRELIMINARY;
QEGMX1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 2. 05-JUL-2004 (TrEMBLrel. 2. 05-JUL-2004 (TrEMBLrel. 2. Hypothetical protein. Homo sapiens (Human).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,

[1] — NUCLEOTIDE SEQUENCE.

NCBI_TaxID=9606;

Homo

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S PRESENTANT OF THE PROPERTY O
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                                                                                                                                                                                                                                                                                             MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A trausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.
A trausher R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
A stapleton M., Soares M.B., Pandldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Hilalon D.K., Muxry D.W., Sodergren B.J., Lu X., Gibbs R.A.,
A hiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
B. Schnerch A., Schnerz J., Jones S.J.M., Marra M.A.,
B. Schnerch A., Schnerz J., Jones S.J.M., Marra M.A.,
B. Schnerch A., Schnerz J., Jones S.J.M., Marra M.A.,
B. Schnerch A., Schnerz J., Jones S.J.M., Marra M.A.,
B. Schnerch A., Schnerz J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       305 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 364
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
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476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;
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SMART; SM00407; IGc1; 3.
SMART; SM00407; IGc1; 3.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 97.0 Matches 225; Conservative
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                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rissum=spleen;
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                  SOW READER A PRESENTATION OF THE PROPERTY OF T
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Hu Z., Garen A.; "Targeting tissue factor on tumor vascular endothelial cells and tumor cells for immunotherapy in mouse models of prostatic cancer."; Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
                                                                                                                          Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
MEDLINE=21477448; PubMed=11593034; DOI=10.1073/pnas.201420298;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hu Z., Garen A.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AF272774; AAK58686.2; -; mRNA.
HSSP; P08709; IKLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0B0023AE70A067A1 CRC64;
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BIRSGNO00005759; Homo sapiens.

GO; GO:0005576; C:extracellular region; IEA.

GO; GO:0004269; F:calcium ion binding; IEA.

GO; GO:0004265; F:chymotrypsin activity; IEA.

GO; GO:0004269; F:trypsin activity; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR000152; Asx. hydroxyl_S.

InterPro; IPR000142; EGF_2.
01-DEC-2001 (TrEMBLrel. 19, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
Factor VII active site mutant immunoconjugate.
Homo sapiens (Human)
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97.0%; Pred. No. 2.6e-74;
live 3; Mismatches 4;
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; PSS0299; IG LIKE; 2.
; PSS0290; IG MHC; UNKNOWN_1.
; PSS0240; TRYPSIN DOM; 1.
; PSS0134; TRYPSIN HIS; UNKNOWN_1.
; PSO0135; TRYPSIN SER; 1.
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SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00010; ASX_HYDROXXL; UNKNOWN_1.
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InterPro), IPR001438; EGF_II.
InterPro), IPR001438; EGF_II.
InterPro), IPR001393; EGF_II.
InterPro), IPR001310; EGF_II.
InterPro), IPR001310; Ig_like.
InterPro), IPR001310; Ig_like.
InterPro), IPR001310; Ig_like.
InterPro), IPR001314; Peptidase_SIA.
InterPro), IPR001254; Peptidase_SIA.
InterPro), IPR001254; Peptidase_SIA.
InterPro), IPR0001254; Peptidase_SIA.
InterPro), IPR0001254; Peptidase_SIA.
InterPro), IPR0001254; Peptidase_SIA.
InterPro), IPR001254; IRR001254; II.
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BGF 3; 1.

BGF 3; 1.

BGF CA; 1.

GLA 1; UNKNOWN 1.

GLA 2; 1.
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PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00010; ECFBLOOD.
PRINTS; PR00001; GLABLOOD.
SMART; SM00179; EGF. CA; 1.
SMART; SM00069; GLA; 1.
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PROSITE;
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BPKSCDKTHICPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF

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PRT;

Q96PQ8 HUMAN PRELIMINARY;

RESULT 13 Q96PQ8 HUMAN ID Q96PO8 HL F. . . .

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Query Match
Best Local Similarity 96.6'
Matches 224; Conservative
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Best Local Similarity
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TISSUB-Peripheral Nervous System;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Astausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;

Altschul S.F.; Zeeberg B., Buecow K.H.; Schaefer C.F.; Bhat N.K.;

Altschul S.F.; Zeeberg B., Buecow K.H.; Schaefer C.F.; Bhat N.K.;

Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;

Astapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;

Brownstein M.J.; Usdin T.B.; Toshiyuki S.; Carninci P.; Prange C.;

A Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullahy S.J.;

Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;

Richards S.; Morley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;

A Willalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;

Fahey J.; Helton E.; Ketteman M.; Madan A.; Rodrigues S.; Sanchez A.;

Multing M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;

Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;

Butterfield Y.S.N.; Krzywinski M.I.; Skalska U.; Smailus D.E.;

Butterfield Y.S.N.; Krzywinski M.I.; Skalska U.; Smailus D.E.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                        567
                                                                                                                              ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 507
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                      NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVIHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                       ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                           NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
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Strausberg R.; AMF61201, -; mRNA.
HSSP; PO1861; 1ADQ.
InterPro; IPR001559; Ig.
InterPro; IPR001559; Ig.
InterPro; IPR003597; Ig.
InterPro; IPR00409; IG.
SMART; SM00400; IGV: I.
PROSITE; PS004095; IG. INTER; 4.
PROSITE; PS004095; IG. INTER; INTERPROSITE; PS004095; IG.
INTERPROSITE; PS0404095; IG.
INTERPROSITE; PS004095; IG.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                            473 AA
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                                                                                                                                                                                                                                                                                                                                                                     QGP055 HUMAN PRELIMINARY;
Q6P055;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Esophagus tumor;
The German cDNA Consortium;
Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                               1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                                                                                                                                                                                                                                                                                                                       362 ISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP
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Score 1221; DB 2; Length 473;
Pred. No. 3e-74;
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Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BX640947; CAE45972.1; -; mRNA.
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Pred. No. 3.1e-74;
3; Mismatches 5;
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                                             3; Mismatches
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INTERPRO; IPR003599; IG-1ike.

INTERPRO; IPR003599; IG-1ike.

INTERPRO; IPR003599; IG-1ike.

INTERPRO; IPR003596; IG-NG.

INTERPRO; IPR003596; IG-NG.

SMART; SM00409; IG; 2.

SMART; SM00409; IG; 2.

SMART; SM00409; IG; 2.

PROSITE; PR00359; IG-LIKE; 4.

PROSITE; PR002909; IG_MHC; UNKNOWN_2.
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05-JUL-2004 (TrEMBLrel. 27, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last ann
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Name-DKFZp686G11190;
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96.6%;
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96.6%;
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QEMZQE HUMAN PRELIMINARY;
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Search completed: November 30, 2005, 00:32:26 Job time : 232 secs

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US-09-428-082B-8

US-09-458-791-8

US-09-458-791-8

US-09-459-066-8

US-09-459-066-8

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US-09-459-066-8

US-09-459-066-8

US-09-955-043A-50

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55.8%; Score 1707; DB 2; Length 3
Best Local Similarity 100.0%; Pred. No. 2e-136;
Matches 320; Conservative 0; Mismatches 0; Indels
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, OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-1
PCT-US95-03866-12
PCT-US95-03866-14
PCT-US96-10043-11
BC-08-472-888A-7
PCT-US96-10043-9
US-08-397-411-7
US-08-773-8718-16
US-08-157-101A-7
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US-08-030-175-41
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US-08-487-550-12
US-09-526-098-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09401636; Patent No. 6913749; GENERAL INFORMATION: APPLICANT: Hellman, Lars T. APPLICANT: Hellman, Lars T.; TITLE OF INVENTION: ENHANCED VACCINES FILE REFERENCE: 10223/006001; CURRENT APPLICATION NUMBER: US/09/401,636; CURRENT FILING DATE: 1999-09-22; PRIOR FILING DATE: 1999-11-02; NUMBER OF SEQ ID NOS: 11; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
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356 ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 415
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Patent No. 6830752
GRNERAL INFORMATION:
APPLICANT: Buyee, Marie-Ange
APPLICANT: Sablon, Erwin
TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
TITLE OF INVENTION: SHOCK,
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
FILE REFERENCE: INNS:015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 GGGSGGGSFTPPTVKILQSSCD----GGGHFPPTIQLLCLVSGYTPGTINITWLED--- 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            332 YTC-----QVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFDLFIRKSPTITCLVVDL 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   294 -------GOVMDVD-----LSTASTTQEGELASTQSELTLSQKHWLSDRT 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       469 -----QGGS-----QVQLVQSGSELKKPGA-----SVKISCKASGYTFTDYGMNWVKQAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGKVEGGGGSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 131;
                                                                                                                                                                                                                                                                                                                                                                                          Length 711;
                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                        41.6%; Score 1273.5; DB 2; 50.1%; Pred. No. 3.5e-99; iive 45; Mismatches 109;
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695 SSYP-----FTFGQG----TKLEIKR 711
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CURRENT FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: PCT/EP 98/05165
PRIOR FILING DATE: 1998-08-14
PRIOR APPLICATION NUMBER: EPO 98870139.7
PRIOR APPLICATION NUMBER: EPO 97870122.5
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1997-08-18
NUMBER OF SEQ ID NOS: 104
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
LENGTH: 711
                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: SYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 286; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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US-10-071-485-90
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Betent No. 6350860
GENERAL INFORMATION
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GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: INTERFERON-Gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
FILE REPERENCE: INNS:015
CURRENT APPLICATION NUMBER: US/09/485,737B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD 125
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                                                                                                           GENERAL INFORMATION:
APPLICANT: WANG Ph.D., Chang Yi
APPLICANT: WANG Ph.D., Chang Yi
TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
TITLE OF INVENTION: ALLERGY
FILE REFERENCE: 11514153US1
CURRENT APPLICATION NUMBER: 08/09/701,623C
CURRENT APPLICATION NUMBER: PCT/US99/13959
PRIOR APPLICATION NUMBER: 09100,287
PRIOR APPLICATION NUMBER: 09100,287
PRIOR FILING DATE: 1999-06-21
PRIOR FILING DATE: 1999-06-21
PRIOR FILING DATE: 1999-06-21
STORMER OF SEQ ID NOS: 91
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
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Pred. No. 6.2e-136;
2; Mismatches 0;
                                                                   ; Sequence 1, Application US/09701623C; Patent No. 6811782
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99.4%;
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Best Local Similarity 99.4
Matches 318; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS: Dorrington,
AUTHORS: Bennich,
JOURNAL: Immunology
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: HUMAN
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PAGES: 3-25
DATE: 1978
                            RESULT 2
US-09-701-623C-1
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50.1%; Pred. No. 3.5e-99;
ive 45; Mismatches 109; Indels 131;
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CURRENT APPLICATION NUMBER: US/10/071,485
CURRENT FILING DATE: 2002-02-03-07
PRIOR APPLICATION NUMBER: 09/485,737
PRIOR PILING DATE: 2000-02-14
PRIOR PILING DATE: 1998-08-14
PRIOR APPLICATION NUMBER: EPO 98870139-7
PRIOR APPLICATION NUMBER: EPO 98870139-7
PRIOR PILING DATE: 1998-06-18
PRIOR FILING DATE: 1997-06-18
PRIOR PILING DATE: 1997-08-18
NUMBER OF SEQ ID NOS: 104
SOFTWARE: Patentin version 3.0
LENGTH: 711
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US-09-428-082B-22
US-09-428-082B-22
Sequence 22, Application US/09428082B
Sequence 22, Application US/09428082B
GENERAL INFORMATION:
APPLICANT: FEIGE, ULRICH
APPLICANT: ELU, CHUNN-FA
APPLICANT: CHEETHAM, JANET C.
                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                             COTHER INFORMATION: SYNTHETIC US-10-071-485-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 50.1
Matches 286; Conservative
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 GVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 DGSPFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK--GGGGGGGTYSC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DXTHICPPCPAPELLGGPSVFLFPPKPXDTIMISRTPEVTCVVVDVSHEDPEVKFNWYVD
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Sequence 8, Application US/09428082B

Sequence 8. Application US/09428082B

Sequence 8. Application

APPLICANT: FILES, ULRICH

APPLICANT: CHEETHAM, JANET C.

APPLICANT: CHEETHAM, JANET C.

APPLICANT: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS

TITLE OF INVENTION: NODIFIED PEPTIDES AS THERAPEUTIC AGENTS

FILE REFERENCE: A-527

CURRENT FILING DATE: 1999-10-22

PRIOR APPLICATION NUMBER: 60/105,371

PRIOR FILING DATE: 1998-10-23

NUMBER OF SEQ ID NOS: 1133

SOFTWARE: PATENTI IN VERBION 3.1

SEQ ID NOS: 1133
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TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS FILE REFERENCE: A-527 CURRENT PEPLICATION NUMBER: US/09/428,082B CURRENT FILING DATE: 1999-10-22 PRIOR APPLICATION NUMBER: 60/105,371 PRIOR PILING DATE: 1998-10-23 NUMBER OF SEQ ID NOS: 1133 SOFTWARE: Patentin version 3.1 SEQ ID NO 22
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                                                                                                                                                                                                                                                                                                                                                                                             Score 1247; DB 2;
Pred. No. 1.5e-97;
7; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Fc-TMP-TMP
US-09-428-0828-8
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: FC-EMP-EMP
US-09-428-082B-22
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Best Local Similarity 81.8%;
Matches 239; Conservative
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Best Local Simil
Matches 232; C
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                                          GVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAK 125
                                                                                                                            126 VQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 185
                                                                                                                                                    122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
                                                                                                                                                                                                              VGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSLSPGKVEGGGGSG---- 240
                                                                                                                                                                                                                                      182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGGIEGPTLRQ 241
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                                                                GVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAK 125
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DKTHICPPCPAPELLGGPSVPLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
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; OTHER INFORMATION: Description of Artificial Sequence: peptide
US-09-422-838C-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
40.6%; Score 1243; DB 2; Length 269;
Best Local Similarity 88.9%; Pred. No. 3.2e-97;
Matches 232; Conservative 5; Mismatches 14; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence Application US/09422838C
Fatent No. 683809
GENERAL INFORMATION:
APPLICANT: Liu, Chuan-Fa
APPLICANT: Peige, Ulrich
APPLICANT: Cheetham, Janet C.
TITLE OF INVENTION: Thrombopoietic Compounds
FILE REPERENCE: 01017/35263
CURRENT APPLICATION INVENT: US/09/422,838C
CURRENT APPLICATION NUMBER: US/09/422,838C
FILE PRIOR FILING DATE: 1999-10-22
FRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 46
SEQ ID NO 46
ILENGTH: 269
                                                                                                                                                                                                                                                                                                  241 ----GGGSGGGGSFTPPTVK 256
                                                                                                                                                                                                                                                                                                                                          242 WLAARAGGGGGGGGIEGPTLR 262
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US-09-181-706-8
S Squence 8, Application US/09181706
Patent No. 6130068
S GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
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                                                                                                                                                                                                                                        40.3%; Score 1232; DB 2; Length 660; 93.0%; Pred. No. 1e-95; ive 7; Mismatches 8; Indels
APPLICANT: Melanie K. Spriggs, Michael R. Comeau, APPLICANT: Robert F. DuBose, Richard S. Johnson TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSE: Janis C. Henry STREET: 51 University St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (206)470-4189
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 660 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 93.0
Matches 227; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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RESULT 9 US-09-458-791-8

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61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
40.3%; Score 1232; DB 2; Length 660;
Best Local Similarity 93.0%; Pred. No. 1e-95;
Matches 227; Conservative 7; Mismatches 8; Indels
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Sequence 8, Application US/09459065
Sequence 8, Application US/09459065
Seturnor 8, Application Security Security Seturation: Springer Melanie Applicant: Springer Melanie TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS: ADDRESSE: Janis C. Henry
VIRAL ENCODED SEMAPHORIN PROTEIN RECEPTOR DNA AND POLYPEPTIDES
                                                                                                                                                                                                                                                               SOFTWARE: Word for Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/459,066
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/958,598
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 263
TELECOMMUNICATION: TELECOMMUNICATION: (206)470-4189
                                                                                                                                                                                                                     COMPOTER READABLE FORM:
MEDIUM TYPE:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/Wil
    TITLE OF INVENTION: VIRAL ENC
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C. Henry
STREET: 51 University St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 660 amino acids
TYPE: amino acid
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MOLECULE TYPE: protein
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                 Sequence o, organizations.
Patent No. 6174689
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
RECEPTOR DNA AND POLYPEPTIDES
                                                                                                                                                                                                                                                               COUNTRY: us
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 10,994
CLASSIFICATION: cUnknown>
PRIOR APPLICATION: cUnknown>
PRIOR APPLICATION WIMBER: 08/958,791
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: HENRY, Janis C
REGISTRATION NUMBER: 24,347
REFERENCE/DOCKET NUMBER: 2631
TELEPAN: (206)233-0644
INFORMATION FOR SEO ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 661 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C. Henry
STREET: 51 University St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09459066
Patent No. 6187909
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
               Sequence 8, Application US/09458791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 93.0
Matches 227; Conservative
                                                                                                                                                                                                                              CITY: Seattle
STATE: WA
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US-09-459-066-8
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US-10-679-999-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92 NWYVDGVEVHNAKTKPREEOYNSTYRVVSVLTVLHODMLNGKEYKCKVSNKALPAPIEKT 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.3%; Score 1232; DB 2; Length 660; 93.0%; Pred. No. 1e-95; ive 7; Mismatches 8; Indels
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8;
                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Dispy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/459,065
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSE: Amgen Inc.
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                    ATJORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REGISTRATION NUMBER: 3631
TELEPHONE: (206)470-4189
TELEPHONE: (206)470-4189
TELEPHONE: (206)470-4189
TELEPHONE: (206)233-0644
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 660 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/958,598
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-679-999-9; Sequence 9, Application US/10679999; Patent No. 6936439; Patent No. 6908439
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51 University St.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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Best Local Similarity
Matches 227; Conserv
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                Seattle
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                                                  COUNTRY:
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121 ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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APPLICANT: FEIGE, ULRICH
APPLICANT: LIU, CHUAN-FA
APPLICANT: LIU, CHUAN-FA
APPLICANT: LIU, CHUAN-FA
APPLICANT: GEETHAM, JAMET C.
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
CURRENT APPLICATION NUMBER: US/09/428,082B
CURRENT APPLICATION NUMBER: 60/105,371
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NO 16
LENGTH: 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1
OTHER INFORMATION: /note= "Met (ATG) starts at SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40.2%; Score 1229; DB 2; 97.0%; Pred. No. 8.2e-96; tive 3; Mismatches 4;
                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/568,528
FILING DATE: 09-May-2000
APPLICATION NUMBER: 09/267,517
FILING DATE: «UNKNOWN:»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                    APPLICATION NUMBER: US/10/679,999
FILING DATE: 06-Oct-2003
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                         NAME: Knight, Matthew W.
REGISTRATION NUMBER: 36,846
REFERENCE/DOCKET NUMBER: A-416
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16, Application US/09428082B
Patent No. 6660843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 379 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 97.0°
Matches 226; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
US-09-428-082B-16
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                                                                                                                                                                                                                                                                                                               62 GVEVHNAKTKPREEGYNSTYRVVSVLTVLAQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
                                                                                                                                                                                                                                                                                                                                                                                                   122 GQPREPQVYTLDPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 VGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGKVEGGGGGGGGG 245
                                                                                                                                                                                                                               2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISKTPEVTCVVVDVSHEDPEVKFNWYVD 61
                                                                                                                                                                                                         6 DKTHTCPPCPAPELLGGPSVFLFPPKPXDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
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Pred. No. 8.7e-96;
3; Mismatches 4; Indels
                                                                                                                         Length 253;
                                                                                                                                                             11, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/595,043A
FILING DATE: 31-JAN-1996
CLASSIFATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER 8
REGISTRATION NUMBER: 32,837
REGISTRATION NUMBER: 32,837
REGISTROCHOOKET NUMBER: SGAR-00371
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQUENCE:
SEQUENCE CHRARACTERISTICS:
LENGTH: 232 amino acids
WUNDER: AMINO acids
WUNDER: AMINO acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233 GGGTY-----SC----HFGP-LTWVCKPQG 252
                                                                                                                     Score 1226; DB 2;
Pred. No. 8.1e-96;
7; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGSFTPPTVKILQSSCDGGGHFPPTIQLLCLVSG 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 50, Application US/08595043A
Patent No. 5935824
GENERAL INFORMATION:
APPLICANT: SGARLATO, GREGORY D.
TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO STATE: CALIFORNIA COUNTRY: UNITED STATES OF AMERICA ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 97.0%;
Matches 225; Conservative
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                       Query Match
Best Local Similarity 84.7%;
Matches 233; Conservative
                                                     CTHER INFORMATION: FC-EMP
US-09-428-082B-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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US-08-595-043A-50
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APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Cecily R
TITLE OF INVENTION: Fe fusion proteins of human granulocyte colony-stimulaing factor
TITLE OF INVENTION: increased biological activities
FILE REFERENCE: 0350N2001
CURRENT APPLICATION NUMBER: US/09/968,362A
CURRENT FILING DATE: 2001-10-01
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.1
SEQ ID NO 26
                                                                                                                  121 ISKAKVOPREPOVYTLPPSRDELTKNOVSLICLVKGFYPSDIAVEWESNGOPENNYKTTP 180
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40.0%; Score 1225; DB 2; Length 232;
Best Local Similarity 97.0%; Pred. No. 8.7e-96;
Matches 225; Conservative 3; Mismatches 4; Indels
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